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RESULT 1
Q9UMV3
ID Q9UM
AC Q9UM
DT 01-M
DT 01-M
DT 01-M
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Maximum
                                                                                                                                                              Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92:
 Q9UMV3;
Q9UMV3;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ned:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             number of
                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lize
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Bd
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length: 2000000000
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Match
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Gapop 60.0 ,
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 ) (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Listing first 500
                                                                                                                                                                                                                                                                                                                                                                                                           SPTREMBL_21:*
                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyright
                                                                                                                                                                                                                                              sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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185
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Created)
Last sequence update)
Last annotation update)
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Q9ULC7
Q9UBP3
Q9UC48
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3 - 2003
                                                                                     ALIGNMENTS
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Q9ulc7
Q9ubp3
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                                                                                                                                                            Description
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RESULT
Q9ULC7
ACCOCC CRAP COCC CRAP COCC
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Best Local
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Q9ULC7;
Q1-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat: Signal.
NON_TER 1
SIGNAL <1
CHAIN 6
            Takahashi M., Fujita T.;

"Partial genomic structure of human MBL-associ
(MASP) 2 (from exon 1 to exon 5).";

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ

1- SIMILARITY: CONTAINS 1 CUB DOMAIN.

EMBL; AB033742; BAA85659.1; -.

HSSP: P00736; 1APQ.
                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00042; CUB; 1.
SMART; SM00179; EGF_CA; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
CCalcium-binding; EGF-like domain; Glycopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-Like.
InterPro; IPR001881; EGF_Ca.
Pfam; PF00431; CUB; 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 structural gene.";
J. Immunol. 162:3481-3490(1999).
-:- SIMILARITY: COMFAINS 1 CUB E
EMBL; Y18282; CAB50729.1; -.
HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MBL-associated serine protease(MASP)-2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MASP-z.
Homo sapiens (Human).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jensenius J.C., Schwaeble W.J.; "Two constituents of the initiation complex of the mannose-binding lectin activation pathway of complement are encoded by a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stover C.M.,
MEROPS;
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             MASP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jensenius J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99192764; PubMed-10092804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mannose binding lectin-associated serine protease-2 related protein, MAp19 (19kDa) precursor (Fragment).
                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
41; Conserv
S01.229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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5
175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thelen M., Lynch N.J.,
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MANNOSE BINDING LECTIN-ASSOCIATED PROTEASE-2 RELATED PROTEIN,. MAP19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (19KDA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41;
Pred. No.
                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474FB56221CD28D1
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                                                                                                                                   MBL-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                          databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lectin;
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                                                                                                                                   protease
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RESULT OPERATE OF ACCORD O
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Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJUNCE FROM N.A.

EQUENCE FROM N.A.

AEDLINE-99262288; PubMed=10330290;

Takahashi M., Endo Y., Fujita T., Matsushita M.;

Takahashi M., Fujita T., Matsushita M.;

Takahashi M., Fujita T., Matsushita M.;

Takahashi M., Fujita T., Matsushita M.;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UBP3;
Q9UBP3;
Q9UBP3;
Q9UBP3;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Mannose binding lectin-associated serine protease-2 related to the protein of the procursor (19 kDa) (MBL-associated protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00431; CUB; 1.

SMART; SM00042; CUB; 1.

SMART; SM00179; EGF_CA; 1.

PROSITE; PS0010; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 1.

Calcium-binding; EGF-1!ke domain; Glycoprotein; Protease;

NON_TER 181 181

181
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InterPro;
InterPro;
                              EMBL;
                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Two constituents of the initiation complex of the mannose-binding lectin activation pathway of complement are encoded by a single structural gene.";
                                                                                               EMBL;
                                                                                                                                                                Submitted (NOV-2000) to the -!- SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99192764; PubMed=10092804; Stover C.M., Thiel S., Thelen M., Lynch Jensenius J.C., Schwaeble W.J.;
                                                                                                                                                                                                                                 "Structure of Human MASP-2
                                                                                                                                                                                                                                                                                                                                                            "Partial genomic structure of human MBL-associated serine (MASP)-2 (from exon 1 to exon 5).";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UBP3
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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[1]
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; Y18284; CAB50731.1; -.
; AB008047; BAA78616.1; -.
; AB033742; BAA85658.1; -.
; Y18281; CAB50728.1; -.
; Y18283; CAB50730.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162:3481-3490(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20171 MW;
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EGF-like.
EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                              Yoon J.;
2 Gene.";
                                                                                                                                                                e EMBL/GenBank/DDBJ
CUB DOMAIN.
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SIGNAL 1
CHAIN 16
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HSSP; P00736; 1APO.
MEROPS; S01.229; -.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR0008561; EGF-1ike.
                                                                                                         "Towards a comprehensive database of propartients with bladder cancer.";
J. Urol. 155:2113-2219(1996)."
SEQUENCE 16 AA: 1751
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SMART; SM00179; EGF_CA; 1.

PROSITE; PS0010; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 1.

Calcium-binding; EGF-like domain; Glycopro
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                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                                     Sequence 1, Application US/09874198 Patent No. US20020082208A1 GENERAL INFORMATION:
APPLICANT: Jensenius, Jens Chr.
APPLICANT: Thiel, Steffen
TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME,
TITLE OF INVENTION: USES FOR IT
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/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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LENGTH: 41
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US-09-874-198-1
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US-09-874-198-2
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APPLICANT: Jensenius, Jens Chr.
APPLICANT: Thiel, Steffen
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PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 60/042,678
PRIOR FILING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
                                                                                                                                                                                                                                                                   Sequence 2, Application US/09874198 Patent No. US20020082208A1
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Patent No. US20020082209A1
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Best Local Similarity
TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, TITLE OF INVENTION: USES FOR IT FILE REFERENCE: 09011-002002 CURRENT APPLICATION NUMBER: US/09/874,198 CURRENT FILING DATE: 2001-06-04 PRIOR APPLICATION NUMBER: 09/054,218 PRIOR APPLICATION NUMBER: 09/054,218 PRIOR FILING DATE: 1998-04-02 PRIOR FILING DATE: 1998-04-03 NUMBER: 60/042,678 PRIOR FILING DATE: 1997-04-03 NUMBER OF SEQ ID NOS: 8
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PRIOR FILING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jensenius, Jens Chr. APPLICANT: Thiel, Steffen
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CURRENT FILING DATE: 2001-06-04
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TYPE: PRT
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Pred. No. 3.6e-35;
Pred. No. 3.6e-35;
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TITLE OF INVENTION: MASS-2 COMPLEMENT-FIXING ENZYME, AND TITLE OF INVENTION: USES FOR IT FILE REFERENCE: 09011-002003

CURRENT APPLICATION NUMBER: US/09/874,238
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR RILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 60/042,678
PRIOR FILING DATE: 1997-04-03
INUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEO ID NO 2
LENGTH: 686
TYPE: PRT
ORGANISM: Homo sapiens
US-09-874-238-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-198-2
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US-09-874-238-2
                                                                                                                                                           Query Match 100.0%; Score 41; DB 10; Length 686; Best Local Similarity 100.0%; Pred. No. 4.2e-34; Matches 41; Conservative 0; Mismatches 0; Indels
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ent No. US20020082209A1
RAL INFORMATION:
LICANT: Jensenius, Jens Chr.
PLICANT: Thiel, Steffen
completed: January 11, 2003, 11:10:13 me : 11 secs
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Title:
Perfect score:
Sequence:
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No.
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Maximum DB seq length: 2000000000
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tches found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ize :
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Score Match Length DB ID
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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41
1 TPLGPKWPEPVFGRLASPGF......GEYANDQERRWTLTAPPGYR 41
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Search completed: January 11, 2003, 11:06:46 Job time : 17 secs

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Mammalia; Eutheria;
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15-JUN-2002 (Rel. 41, Last annotation update)
Mannan-binding lectin serine protease 2 precursor (EC 3.4.21.-)
(Mannose-binding protein associated serine protease 2) (MASP-2)
                                                                                                                                                                                                                                                                            S2_HUMAN STANDARD;

00187; 075754; 094270; 09B2H0;

070.00 (Rel 39, Created)

30-MAY-2000 (Rel 39, Last sequents)

15-JUN-2002 (Rel 41, Last anno
SEQUENCE FROM N.A
                         "A second serine protease associated with mannan-binding lectin that activates complement.";
Nature 386:506-510(1997).
                                                                  MEDLINE-97242412; PubMed-9087411; Thiel S., Jensen T.V., Stover C.M., Scousen K., Willis A.C., Eggleton P., Reid K.B.M., Jensenius J.C.;
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=9606;
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length: 2000000000
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Match Length DB
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Catarrhini; Hominidae;
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PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00032; CCP; 2.
SMART; SM00042; CUB; 2.
SMART; SM00042; EGF_CA; 1.
SMART; SM00070; Tryp_SPc; 1.
PROSITE; PS001010; ASX_HYDROXYL; 1
PROSITE; PS01180; CUB; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00135; TRYPSIN_HIS; FAI
PROSITE; PS00134; TRYPSIN_HIS; FAI
PROSITE; PS00134; TRYPSIN_HIS; FAI
PROSITE; PS00135; TRYPSIN_EGR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thiel S., Vorup-Jensen T., Stover C.M., SCHWGELL, Poulsen K., Willis A.C., Eggleton P., Hansen S., Holmskov U Reid K.B.M., Jensenius J.C.;
*Identification and characterization of a novel protein of incommon system, mannan-binding lectin-associated serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

-: FUNCTION: TRYDSIN PROTEASE THAT PRESUMABLY PLAYS AN IMPORTANT ROLE
-: FUNCTION: TRYDSIN PROTEASE THAT PRESUMABLY PLAYS AN IMPORTANT ROLE
-: SIMILARITY: CLEAVES C4 GENERATING C4A AND C4B.
-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-: SIMILARITY: CONTAINS 2 SUSHI (SCD) DOMAINS.
-: SIMILARITY: CONTAINS 2 CUB DOMAINS.
-: SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                             Pfam; PF00084; sushi; 2. Pfam; PF00089; trypsin; 1. Pfam; PF00431; CUB; 2.
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                                                                                                                                                                                                                                                                                                                                                                                MIM; 605102;
                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:6902;
                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          structural gene.";
J. Immunol. 162:3481-3490(1999).
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Stover C.M., Thiel S., Thelen M., Lynch N.J., Vorup-Jensen T.,
Jensenius J.C., Schwaeble W.J.;
"Two constituents of the initiation complex of the mannan-binding
lectin activation pathway of complement are encoded by a single
                                                                                                                                                                                                                                                              InterPro;
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"Structure of human MASP-2 gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                          AF321562; AAG50274.1;
AF321558; AAG50274.1;
AF321559; AAG50274.1;
AF321560; AAG50274.1;
AF321561; AAG50274.1;
AF321561; AAG50274.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                P00763;
                                                                                                                                                                                                                                                                                                                            IPR000152; Asx_hydroxyl.
IPR000859; CUB_domain.
IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                             IPR000561; EGF-like.
IPR001881; EGF_Ca.
IPR001254; Ser_protease_Try.
IPR000436; Sushi_SCR_CCP.
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100.0%; Pred. No. 2.9e-34;
n. Mismatches 0;
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D -> Y (IN REF. 4).
L -> LCS (IN REF. 4).
G -> E (IN REF. 4).
G -> E (IN REF. 3).
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L -> LIL (IN REF. 3).
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SUSHI 2.
SUSHI 2.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
HYDROXYLATION (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                            Length 686;
                                                                                                                                                                                                                                                   Indels
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C:Accession: A59271

R:Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, I wature 386, 506-510, 1997

A;Title: A second serine protease associated with mannan-binding lectin that activates A;Reference number: A59271; MUID:97242412; PMID:9087411

A;Accession: A59271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N;Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                A;Cross-references: GB:Y09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007627
A;Experimental source: tissue liver
A;Note: submitted to GenBank, December 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
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                                                            A; Gene: GDB: MASP2
                                                                                                            A; Note:
                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-686 <JEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
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                                                                                                                                                                                                                                                                       A; Status: nucleic acid sequence not shown; not compared with conceptual translation
;Cross-references: GDB:6071500;Map position: 1p36.2-1p36.3
                                                                                     ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                    parts of this sequence, including the amino end of the mature protein, were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Score Match Length DB ID
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41
1 TPLGPKWPEPVFGRLASPGF......GEYANDQERRWTLTAPPGYR
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Copyright (c) 1993 - 2003 Compu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              686
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                                                                                                                                                                                                                                                                                                                                                                                                                                      F:19-134/Domain: Clr/Cls repeat homology <ClR1>
F:142-180/Domain: EGF homology <EGFP>
F:144-293/Domain: Clr/Cls repeat homology <ClR2>
F:184-93/Domain: Clr/Cls repeat homology <ClR2>
F:300-361/Domain: complement factor H repeat homology <FH1>
F:366-430/Domain: complement factor H repeat homology <FH2>
F:445-679/Domain: trypsin homology <TRY>
F:445-679/Domain: trypsin homology <TRY>
F:72-90/142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement facto C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serin F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
Search completed: January 11, Job time : 20 secs
                                                                                                                                                                                                                                                                                                                                                        F;483,532,633/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                    F;158/Modified site: erythro-beta-hydroxyasparagine (Asn) *status F;444-445/Cleavage site: Arg-Ile (autolytic) *status predicted
                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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                                                                                                                                                  TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                  TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR
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                           2003, 11:06:16
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Pred. No. 6.7e-35;
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Result
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Maximum DB
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                                                                                                                                       Score
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seq length: 2000000000
             4141
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Match Length
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         100.0
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1 TPLGPKWPEPVFGRLASPGF......GEYANDQERRWTLTAPPGYR
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                                                                                                                                                                                                                                                                                                                      I: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980_DAT: *
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980_DAT: *
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991_DAT: *
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991_DAT: *
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Copyright (c) 1993 - 2003
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/SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
      41
671
686
686
1034
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    AAE14563
AAE14565
AAE14564
AAE14568
ABG21134
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                        Human
Human
                                                                                                                                  Description
                                                                   Human 20 kDa MASP-
Human mature MASP-
n MASP-2 prote
n MASP-2 prote
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ALIGNMENTS

17-MAY-2002

(first entry)

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AAE14565
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AAE14563
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                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                        The invention relates to use of a polypeptide derived from mannan-binding lectin (MBL) associated serine protease-2 (MASP-2) for producing a pharmaceutical composition MASP-2 is a complement-fixing enzyme and involved in lectin pathway of complement activation. The pharmaceutical composition comprising MASP-2 is useful for treating infections caused by microbes such as fungus, yeast, retrovirus (e.g. human immunodeficiency virus (HIV)), or pathogenic bacteria which are resistant to at least one antibiotic medicament or multiresistant. The polynucleotide encoding MASP-2 is useful for treating patients deficient in MASP-2. The invention also discloses MASP-2 assays which are useful for determination of MASP-2 activity or
                                                                                                                                                                                                                                                                                              levels in patients suffering from e.g. infections, inflammatory disorders and spontaneous recurrent abortion. The pharmaceutical composition comprising MASP-2 inhibitor is useful for treating inflammatory disorders. The present sequence is human MASP-2 20 kDa fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for mannan-binding lectin associated, to treat bacterial, fungal,
                             AAE14565;
                                                           AAE14565 standard;
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 39; Page 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUL-2000; 2000DK-0001089
01-JUN-2001; 2001DK-0000870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE14563;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human immunodeficiency virus; pathogenic bacteria; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human 20 kDa MASP-2 fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jensenius JC, Thiel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (THIE/) THIEL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUL-2001; 2001WO-DK00499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JENS/) JENSENIUS J C.
                                                                                                                                                                   1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                       41 AA;
                                                                                                                                                                                                       Conservative
                                                         peptide; 671 AA
                                                                                                                                                                                                                 100.0%; Score 41; 100.0%; Pred. No.
                                                                                                                                                                                                     0;
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                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                 1.1e-34;
                                                                                                                                                                                                                                   DB 23;
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                                                                                                                                                                                                                                   Length 41;
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                                                                                                                                                                                                    Gaps
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Human mature MASP-2 protein.

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RESULT 3
AAE14564
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                                                                                                                                                                                                                                                                                                                                                    The invention relates to use of a polypeptide derived from commanishing the protesser 2 (MASP-2) for commanishing lectin (MBL) associated serine protease-2 (MASP-2) for composition. MASP-2 is a complement activation. CC fixing enzyme and involved in lectin pathway of complement activation. CC The pharmaceutical composition comprising MASP-2 is useful for cc treating infections caused by microbes such as fungus, yeast, cc extraorirus (e.g. human immunodeficiency virus (HIV)), or pathogenic cc multiresistant. The polynucleotide encoding MASP-2 is useful for cc multiresistant. The polynucleotide encoding MASP-2 is useful for creating patients deficient in MASP-2. The invention also discloses MASP-2 assays which are useful for determination of MASP-2 activity or evels in patients suffering from e.g. infections, inflammatory disorders and spontaneous recurrent abortion. The pharmaceutical composition comprising MASP-2 inhibitor is useful for treating inflammatory cc disorders. The present sequence is human mature MASP-2 protein.
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 41; Conserv
Human MASP-2 protein
                                                                                                 AAE14564 standard;
                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for producing pharmaceutical composition, to treat bacterial, fungal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JENS/) JENSENIUS J C. (THIE/) THIEL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion; human immunodeficiency virus; pathogenic bacteria; inflammatory disorder.
                                 17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jensenius JC, Thiel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUL-2001; 2001WO-DK00499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200206460-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3-JUL-2000; 2000DK-0001089
1-JUN-2001; 2001DK-0000870
                                                                                                                                                                                      1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                          \vdash
                                                                                                                                                                                                            TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page
                                                                                                                                                                                                                                                                                                                           671 AA;
                                                                                                                                                                                                                                                            Conservative
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "This region is specifically claimed claim 45\,^{\rm m}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 15..671
                                                                                                   Protein;
                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76pp; English
                                                                                                   686
                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                        Score 41; DB 23;
Pred. No. 1.2e-33;
                                                                                                                                                                                                                                                          Mismatches
                                                                                                   AA
                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                          Length 671;
                                                                                                                                                                                                                                                          Indels
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Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion; human immunodeficiency virus; pathogenic bacteria; inflammatory disorder.
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Homo sapiens.

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Active-site
Active-site
Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for producing pharmaceutical composition, to treat bacterial, fungal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded by CA" Misc-difference 156
                                                                                                                                                                       13-JUL-2000;
01-JUN-2001;
                                                                                                                                                                                                              13-JUL-2001; 2001WO-DK00499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
Misc-difference 155
                                                                                               Jensenius JC,
                                                                                                                                                                                                                                                                       WO200206460-A2.
                                                                                                                                                                                                                                                                                                                                                         Domain
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                                                                                                                           (JENS/) JENSENIUS J C.
(THIE/) THIEL S.
                                                       2002-179791/23.
DB; AAD24224.
                                                                                                                                                                     2000DK-0001089.
2001DK-0000870.
                                                                                                 Thiel
                                                                                                                                                                                                                                                                                              /label=
483
532
633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Fragment obtained by amino acid
of peptides"
                                                                                                                                                                                                                                                                                                                                                        445..468
                                                                                                                                                                                                                                                                                                                                                                                    432.
                                                                                                                                                                                                                                                                                                                                                                                                                            410.
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16..31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138..296
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                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Fragment obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= Clr/Cls-like_domain
                                                                                                                                                                                                                                                                                                                                                                                                                            peptides'
0..417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Encoded by
                                                                                                                                                                                                                                                                                                                                                                  "Linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complement control protein domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Fragment obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "This region is specifically claimed in
                                                                                                                                                                                                                                                                                                                                        Serine_protease_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region is specifically claimed in claim 41.0 to 296 is specifically claimed in claim 47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is specifically claimed in claim 46"
                                                                                                                                                                                                                                                                                                                                                                                                            by amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to use of a polypeptide derived from mannan-binding lectin (MBL) associated serine protease-2 (MASP-2) for CC producing a pharmaceutical composition. MASP-2 is a complement-CC fixing enzyme and involved in lectin pathway of complement activation. The pharmaceutical composition comprising MASP-2 is useful for treating infections caused by microbes such as fungus, yeast, cc retrovirus (e.g. human immunodeficiency virus (HIV)), or pathogenic Dacteria which are resistant to at least one antibiotic medicament or CC multiresistant. The polynucleotide encoding MASP-2 is useful for CC treating patients deficient in MASP-2. The invention also discloses CC MASP-2 assays which are useful for determination of MASP-2 activity or CC levels in patients suffering from e.g. infections, inflammatory disorders and spontaneous recurrent abortion. The pharmaceutical composition CC comprising MASP-2 inhibitor is useful for treating inflammatory disorders. The present sequence is human MASP-2 protein.
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Best Local S
Matches 41
                                                                                                                                                                                                      /note= "Encoded Misc-difference 298
                                                                                                                                                                                                                                        /note= "Encoded by Misc-difference 156
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion; human immunodeficiency virus; pathogenic bacteria; inflammatory disorde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE14568 standard; Protein; 686
                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                         /label- Mature_MASP-2_protein Misc-difference 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human MASP-2 protein, alternative version.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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              13-JUL-2000; 2000DK-0001089
01-JUN-2001; 2001DK-0000870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAY-2002
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                                                                                                                                     WO200206460-A2
                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                13-JUL-2001; 2001WO-DK00499
                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ote: The present sequence is stated as being the same as EQ ID NO:2 shown in sequence listing of the specification (AAE14568) However the sequences differ at various locations.
                                                                                                                                                                                                                                                                                                                                                                                                                omo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     686 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                  /note= "Encoded by CAG" 299
                                                                                                                                                                                                                                                                                                                             /label= Signal_peptide
16..686
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                  "Encoded by CCT'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 23;
Pred. No. 1.2e-33;
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Best Local Similarity
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                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to use of a polypeptide derived from mannan-binding lectin (MBL) associated serine protease-2 (MASP-2) for producing a pharmaceutical composition. MASP-2 is complement-fixing enzyme and involved in lectin pathway of complement activation. The pharmaceutical composition comprising MASP-2 is useful for treating infections caused by microbes such as fungus, yeast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for producing pharmaceutical composition, to treat bacterial, fungal,
                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                         ABG21134 standard; Protein; 1034 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 41; Page 71-73; 76pp; English.
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                                                                               31-MAR-2000;
23-AUG-2000;
                                                                                                                                30-MAR-2001; 2001WO-US08631
                                                                                                                                                                  11-OCT-2001
                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #21125
                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002 (first entry)
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(THIE/) THIEL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              686 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                               2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 41; DB 23; 100.0%; Pred. No. 1.2e-33;
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cc polymertide (II) sequences. (I) is useful as hybridisation probes, cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags (CC for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical maging of sites expressing (II). (I) and (II) are useful for treating isorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations in CC cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC and contain a cid sequences. ABG00010-ABG30377 represent novel human CC Note: The sequence data for this pattent did not appear in the printed specification, but was obtained in electronic format directly from WIPO CC at ftp. wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                QΥ
Search completed: January 11, 2003, 11:04:36 Job time : 36 secs
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 41; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID No 51493; 103pp; English.
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N-PSDB; AAS85321.
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                                                                                                                                 752 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 792
                                                                                                                                                                    1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                       1034 AA;
                                                                                                                                                                                                                                                                  0; Mismatches
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Pred. No. 1.7e-33;
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Result
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hed:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    number of hits satisfying chosen parameters:
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1: /cgn2_6/ptodata/2/pubpaa/U
2: /cgn2_6/ptodata/2/pubpaa/U
3: /cgn2_6/ptodata/2/pubpaa/U
4: /cgn2_6/ptodata/2/pubpaa/U
5: /cgn2_6/ptodata/2/pubpaa/U
6: /cgn2_6/ptodata/2/pubpaa/U
6: /cgn2_6/ptodata/2/pubpaa/U
9: /cgn2_6/ptodata/2/pubpaa/U
10: /cgn2_6/ptodata/2/pubpaa/U
11: /cgn2_6/ptodata/2/pubpaa/U
11: /cgn2_6/ptodata/2/pubpaa/U
13: /cgn2_6/ptodata/2/pubpaa/U
14: /cgn2_6/ptodata/2/pubpaa/U
15: /cgn2_6/ptodata/2/pubpaa/U
16: /cgn2_6/ptodata/2/pubpaa/U
17: /cgn2_6/ptodata/2/pubpaa/U
18: /cgn2_6/ptodata/2/pubpaa/U
19: /cgn2_6/ptodata/2/pubpaa/U
11: /cgn2_6/ptodata/2/pubpaa/U
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13.482 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-874-198-1
238
1 TPLGPKWPEPVFGRLASPGF......GEYANDQERRWTLTAPPGYR 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
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Listing first 60 summaries
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Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                    Length
   US-09-799-118-6
US-09-925-302-611
US-09-919-497-89
                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 20, Appli
Sequence 20, Appl
Sequence 21, Appl
Sequence 24, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 89, Appli
Sequence 89, Appli
Sequence 89, Appli
Sequence 87, Appli
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	e 7, e 128 e 128 e 129 e 14, p e 102 e 8, p e 8, p e 8, p e 3, p e 4, p e 6, p

## ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/874,198
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR ETLING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 60/042,678
PRIOR FILING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                             ; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-198-1
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09874198
Patent No. US20020082208A1
GEMERAL INFORMATION:
APPLICANT: Jensenius, Jens Chr.
APPLICANT: Thiel, Steffen
TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING
TITLE OF INVENTION: USSS FOR IT
FILE REFERENCE: 09011-002002
Query Match
Best Local Similarity
Matches 41; Conserv
100.0%; Score 238; DB 10; milarity 100.0%; Pred. No. 5.1e-22; Conservative 0; Mismatches 0;
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    Indels
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RESULT 4
                                                                                                                                                                                                                                                                  SEQ ID NO 2
LENGTH: 686
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SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1
                                                                                                                                  Matches
                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09874198 Patent No. US20020082208A1
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Best Local Similarity
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RENT APPLICATION NUMBER: US/09/874,198

RRENT FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: 09/054,218

PRIOR FILING DATE: 1998-04-02

PRIOR APPLICATION NUMBER: 60/042,678

PRIOR APPLICATION NUMBER: 60/042,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jensenius, Jens Chr. APPLICANT: Thiel, Steffen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/874,238
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
OR APPLICATION NUMBER: 60/042,678
OR FILING DATE: 1997-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thiel, Steffen
TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING
TITLE OF INVENTION: USES FOR IT
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING TITLE OF INVENTION: USES FOR IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jensenius, Jens Chr. APPLICANT: Thiel, Steffen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 09011-002003
                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 41
TYPE: PRT
                                                                                                                                                   Local Similarity
                                                       16
                                                                                          1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
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                                                     TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 56
                                                                                                                                  41;
                                                                                                                                  Conservative
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                                                                                                                                                 100.0%;
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                                                                                                                            Score 238; DB 10;
Pred. No. 1.1e-20;
Mismatches 0;
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Pred. No. 5.1e-22;
Mismatches 0;
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                                                                                                                                Indels
                                                                                                                                                                 Length
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US-09-874-198-6

Sequence 6, Application US/09874198 Patent No. US20020082208A1 GENERAL INFORMATION:

APPLICANT: Jensenius, Jens Chr. APPLICANT: Thiel, Steffen

TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, TITLE OF INVENTION: USES FOR IT

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В
                                                                                                                                         ; NAME/KEY: SITE ; LOCATION: (70) CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-853-563
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-764-853-563; Sequence 563, Application US/09764853; Patent No. US20020099672A1
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                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 563
LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
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LENGTH: 686
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                                                                                     Query Match
Best Local
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                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                     Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 09011-002003
CURRENT APPLICATION NUMBER: US/09/874,238
CURRENT FILING DATE: 2001-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 60/042,678
PRIOR FILING DATE: 1997-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, TITLE OF INVENTION: USES FOR IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jensenius, Jens Chr. APPLICANT: Thiel, Steffen
                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 PXWDSKEPVCIAACGGVIRNATTGRIVSPGFPGNYSNNLTCHWLLEAPEGQR 120
                               5 PKW--PEPV------FGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                    Conservative
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                                                                                     39.3%;
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                                                                                   Score 93.5; DB 10 Pred. No. 0.00028;
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Pred. No. 1.1e-20;
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                                                                  Mismatches
                                                                                                     DB 10;
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                                                                    Indels
                                                                                                    Length 174;
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FILE REFERENCE: 09011-002002

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RESULT 8
US-10-004-551-18
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                                                                                                                                                                                              Sequence 18, Application US/10004551
Publication No. US20030004310A1
GENERAL INFORMATION:
APPLICANT: SHIMEDTS, RICHARD A
APPLICANT: FERNANDES, ELMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 14; Conserv
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SEQ ID NO 6
LENGTH: 679
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                                                                                        APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
CURRENT APPLICATION NUMBER: US/10/004,551
CURRENT FILING DATE: 2001-12-05
CURRENT FILING DATE: 2001-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND TITLE OF INVENTION: USES FOR IT FILE REFERENCE: 09011-002003
CURRENT APPLICATION NUMBER: US/09/874,238
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR APPLICATION NUMBER: 60/042,678
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1997-04-03
NUMBER: 05-560, ID NOS: 8
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
                                                             PRIOR APPLICATION NUMBER: 09/635,949 PRIOR FILING DATE: 2000-08-10
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CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 45.2 ies 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            8 MFGQIQSPGYPDSYPSDSEVTWNITVPDGFR 38
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45.2%;
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Pred. No. 0.0014;
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NUMBER OF SEQ ID NOS: 110
SCOTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 22, Application US/10004551
Publication No. US20030004310A1
GENERAL INFORMATION:
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Best Local Similarity
Watches 21; Conserv:
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; ORGANISM: Homo sapiens
; OTHER INFORMATION: n 2077 can be A, G,
US-10-004-551-18
                                                                                                                 US-10-004-551-22
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SEQ ID NO 20
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: n 2077 can be A, G,
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Matches
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                                                                                 Query Match
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
                                                                                                                                                                                                                                                                                         APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
                                                                                                                                                                                                                                                                                                                          APPLICANT: SHIMKETS, RICHARD A APPLICANT: FERNANDES, ELMA
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PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
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CURRENT FILING DATE: 2001-12-05
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                                                 Local Similarity
les 21; Conserv
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les 21; Conserv
5 PKW--PEPV------FGRLASPGFPGEYANDQERRWTLTAPPGYR 41
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                                                               38.4%;
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                                                             Score 91.5; DB 9
Pred No. 0.0016;
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Length 994;

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US-10-004-551-16
; Sequence 16, Application US/10004551
; Publication NO. US20030004310A1
; GENERAL INFORMATION:
; APPLICANT: SHIMKETS, RICHARD A
; APPLICANT: FERNANDES, ELMA
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
TMBER OF SEQ ID NOS: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SHIMKETS, RICHARD A
APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: 15966-559
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APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
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CURRENT FILING DATE: 2001-12-05
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
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                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
OTHER INFORMATION: n 1755
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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THER INFORMATION: n 2093 can be A,
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Pred. No. 0.0016;
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Pred. No. 0.0032;
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US-10-041-406-5
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US-09-886-429-4
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                  SEQ ID NO 5
LENGTH: 144
                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Bandaru,
                                                                                                                                                                                                                                                                           Sequence 5, Application US/10041406 Patent No. US20020164705A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4 LENGTH: 144
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                                                                                                                                  FILE REFERENCE: 10448-130001
CURRENT APPLICATION NUMBER: US/10/041,406
CURRENT FILING DATE: 2002-01-08
                                                                                                                                                                                   TITLE OF INVENTION: 39362, A NOVEL CUB DOMAIN CONTAINING TITLE OF INVENTION: PROTEIN FAMILY MEMBER AND TOTAL FILE BEDEFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/886,429
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/213,963
PRIOR FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 56739, A NOVEL CUB DOMAIN CONTAINING
TITLE OF INVENTION: PROTEIN AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/004,551
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
                                                                                               PRIOR APPLICATION NUMBER: 60/: PRIOR FILING DATE: 2001-01-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 15966-559
                                                         SOFTWARE: FastSEQ for Windows Version 4.0
                                                                               NUMBER OF SEQ ID NOS: 9
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OTHER INFORMATION: n 1755 can be A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                             16 GTITSPNYPNSPSGESYPNNLECVWTISAPPGYR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                    13 GRLASPGFP----GE-YANDQERRWTLTAPPGYR 41
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                                                                                                                  60/260,286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 81.5; DB Pred. No. 0.006;
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Pred. No. 0
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Query Match
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                              RESULT 17
US-09-925-302-611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 16
US-09-799-118-6
                                                                                                                                                                                                                                 US-09-799-118-6
Sequence 611, Application US/09925302 Patent No. US20020044941A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09799118
Patent No. US20020090708A1
**ENERAL INFORMATION:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 GTITSPNYPNSPSGESYPNNLECVWTISAPPGYR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 GRLASPGFP----GE-YANDQERRWTLTAPPGYR 41
                                                                                                   7
                                                                                                                              8 PEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lee, Tae Ho
Wisniewski, Hans Georg
                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Cytokine-Induced Protein,
Therefor and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                            PQKLFGEVTSPLFPKPYPNNFETTTVITVPTGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/799,118 FILING DATE: 06-Mar-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/242,097 FILING DATE: 13-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C.
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                                                                                                                                                                                                                                                                                                                            LENGTH: 101 amino acids
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Pred. No. 0.0047
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Pred. No. 0.006;
5; Mismatches
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                                                                                                                                                                                            Length 101;
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RESULT 19
US-09-874-198-7
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Sequence 89, Application US/09919497
Patent No. US20020106662A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens US-09-919-497-89
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GENERAL INFORMATION:
APPLICANT: Jensenius, Jens Chr.
APPLICANT: Thiel, Steffen
TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND
TITLE OF INVENTION: USES FOR IT
                                                                                                    Sequence 7, Application US/09874198 Patent No. US20020082208A1
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 89
LENGTH: 449
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Best Local Similarity 44.1%;
Matches 15; Conservative
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LENGTH: 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2001-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MUTTER, GEORGE L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PA104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR EILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: B0801/7225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE LOCATION: (307)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                        28 PNYTRPVFLCGGDVKGESGYVASEGFPNSYPPNKECIWTITVPEG
                                                                                                                                                                                                                                                             5 PKWPEPVF-----GRLASPGFPGEYANDQERRWTLTAPPG 39
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Pred. No. 0.023;
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Sequence 7. Application US/09874238

Patent No. US20020082209A1

GENERAL INFORMATION:
APPLICANT: Jensenius, Jens Chr.
APPLICANT: Jensenius, Jens Chr.
APPLICANT: Thiel, Steffen

TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND TITLE OF INVENTION: USES FOR IT

FILE REFERENCE: 09011-002003

CURRENT APPLICATION NUMBER: US/09/874,238

CURRENT APPLICATION NUMBER: 09/054,218

PRIOR APPLICATION NUMBER: 09/054,218

PRIOR APPLICATION NUMBER: 60/042,678

PRIOR APPLICATION NUMBER: 60/042,678

PRIOR FILING DATE: 1997-04-03

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 688

TYPE: PRT

ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/874,198
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 60/042,678
PRIOR FILING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 688
TYPE: PAT
ORGANISM: Homo sapiens
US-09-874-198-7
Search completed: January 11, 2003, 11:03:49 Job time : 61 secs
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US-09-874-238-7
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Best Local Similarity 44.1%;
Matches 15; Conservative
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Local Similarity 44.1%;
hes 15; Conservative
                                                                                 8 PEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41 |: :|| :|| :|| :|| :||
                                                                                                                                                                   Score 81; DB 10; Length 688; Pred. No. 0.037; 5; Mismatches 14; Indels
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries
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Maximum DB seq
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2: /cgn2_6/ptodata/1.
3: /cgn2_6/ptodata/1.
4: /cgn2_6/ptodata/1.
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length: 2000000000
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1 TPLGPKWPEPVFGRLASPGF......GEYANDQERRWTLTAPPGYR
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-872-757-4
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US-08-917-473-4
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US-08-872-757-4
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US-08-866-650-5
US-08-911-408-2
US-09-240-473-3
US-09-240-473-3
US-09-031-523-3
US-09-031-523-3
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(without alignments)
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Compugen Ltd
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6 Appli

9 Appli

9 Appli

9 Appli

8 Appli

8 Appli

8 Appli

8 Appli

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ALIGNMENTS 350B-2 2, Application US/08470350B 0. 5684126 INFORMATION: CANT: Li, Xiao	22.3	2	٧,	υ N	٧.	2	2	2	٠.	٠.		٠.	4	4.	4 .	<u>ت</u> .	лυ	٠.	5	5	5	5	5			5			6	<u>.</u>		
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Sequence 2, Application US/08470350B
Patent No. 5684126
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: L1, Xiao
APPLICANT: Snyder, Solomon H
TITLE OF INVENTION: Ebnerin: A Secreted von Ebner's Gland
TITLE OF INVENTION: Protein Associated with Taste Buds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSteent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,350B
FILLING DATE:
CLASSIFICATION NUMBER: US/08/470,350B
FILLING DATE:
NAME: Wolffe, Susan A
REGISTRATION NUMBER: 33,568
REGISTRATION TORORMATION:
TELEPHONE: 202-508-9100
TELEPHONE: 202-508-9100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

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US-09-206-695-6
; Sequence 6, Application
; Sequence 10210905
; Patent No. 6210905
; GENERAL INFORMATION:
; APPLICANT: Lee, Tax
; APPLICANT: Wisniews
                                                                                                                                                        B
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                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: US-08-242-097-6
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity 31.4
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/242,097
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25.618
REFERENCE/DOCKET NUMBER: LEE26/VILCEK-1B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08242097
Patent No. 5846763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: Lee, Tae Ho
PPLICANT: Wishlewski, Hans Georg
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding
TITLE OF INVENTION: Therefor and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clii
STATE: L.
TD: 20004
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                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-737-3528 ORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          825 GPVWTSPPFVNYTCGGFLTGLSGQFSSPYYPGSYPNNARCLWNIEVPNNYR 875
                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                        7
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                                                                                                                                                       PQKLFGEVTSPLFPKPYPNNFETTTVITVPTGYR 40
                                                                                                                                                                                      PEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
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                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                    Application US/09206695
                                                                                                                                                                                                                                                                                                                                                                           101 amino acids
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419 Seventh Street, N.W.,
   Wisniewski, Hans Georg
                                                                                                                                                                                                                        Conservative
                   Lee, Tae Ho
                                                                                                                                                                                                                                                                                                                            linear
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Pred. No.
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Pred. No. 0.022;
5; Mismatches 17;
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suite 300
                                                                                                                                                                                                                                        DB 2;
0.0027;
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                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                           APPLICANT:
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/242,097 FILING DATE: 13-MAY-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             TITLE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                             COUNTRY:
             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/206,695 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 419 Sever CITY: Washington
                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 212-628-5197
TELEFAX: 212-737-3528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 PEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
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                                                                               19406
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Young, Peter R
Yue, Tian-Li
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419 Seventh Street, N.W., Suite 300
                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                          McNulty, Dean E
Rosen, Craig A
                                                                                                                                                                                                                                                                                                         McDonnell,
                                                                                                                                                                                                                                                                                                                           Hurle, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytokine-Induced Protein, TSG-6, DNA Coding Therefor and Uses Thereof
                                                                                                                                                                                                                                                                                                            Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25,618
                                                                                                                                                            Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 81; I
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
0.0027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 101;
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US-08-839-008-2
; Sequence 2, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
 TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/56
FILING DATE: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS.
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Young, APPLICANT: Yue, Ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
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CITY: F
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TOPOLOGY: lir
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             REFERENCE/DOCKET NUMBER: P50
LECOMMUNICATION THE
                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 23-APR-1997
                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                        COUNTRY: U:
ZIP: 19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
                                       NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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TELEPHONE:
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17; Conserv
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McNulty, Dean E
Rosen, Craig A
Siemens, Ivo R
Young, Peter R
Yue, Tian-Li
                                                                                                                                                                                                                                                    USA
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                          08/563,697
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Pred. No.
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Best Local Similarity
Matches 17; Conserv
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                                                                             PARLIER
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TOPOLOGY: lin
MOLECULE TYPE:
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                                                                           FILING DATE:
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SEQUENCE CHARACTERISTICS
28 PNYTRPVFLCGGDVKGESGYVASEGFPNLYPPNKECIWTITVPEG 72
                5 PKWPEPVF------GRLASPGFPGEYANDQERRWTLTAPPG 39
                                                                                                                                                                                     449 amino acids
                                                        Conservative
                                                                                                                              protein
                                                                                                                                                       single
                                                                     32.8%;
                                                        5; Mismatches
                                                                     Score 78; DB 2; Pred. No. 0.034;
                                                                                   DB 2;
                                                       13; Indels
                                                                                 Length 449
                                                        10;
                                                        Gaps
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EARLIER APPLICATION NUMBER: PCT/US98/1368
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER APPLICATION NUMBER: 60/051,932 CURRENT APPLICATION NUMBER: US/09/227,357 CURRENT FILING DATE: 1999-01-08 FILE REFERENCE: PZ010P1 APPLICATION NUMBER: 60/0 APPLICATION NUMBER: 60/ FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/ FILING DATE: 1997-07-08 APPLICATION NUMBER: FILING DATE: 1997-0 FILING DATE: 1997-07-08 FILING DATE: 1997-0 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: 60/051,918 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: Fischer et al Application US/09227357 123 Human Secreted Proteins NUMBER: 60/051,928 1997-07-08 1997-07-08 1997-07-08 1997-07-08 1997-08-18 1997-08-18 1997-07-08 1997-07-08 1997-08-18 60/052,733 60/051,920 60/051,919 60/052,795 60/051,930 PCT/US98/13684 60/055,949 60/055,948 60/055,723 60/055,722 60/055,953

APPLICATION NUMBER: 60/1 FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/1 FILING DATE: 1997-08-18

60/055,964 8-18 60/056,360

APPLICATION NUMBER: 60/055,947 FILING DATE: 1997-08-18

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US-08-839-008-5
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Best Local Similarity
Matches 15; Conserv
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TYPE: PRT
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
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APPLICANT: McDonn
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                                                                                                                                                                                                                                                                                                                                                                                                           nt No.
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BER OF SEQ ID NOS: 672
                                                                                                                                           ADDRESSEE: SmithKline
STREET: 709 Swedeland
CITY: King of Prussia
STATE: PA
                                                                                                                   COUNTRY: U:
ZIP: 19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 FGRLASPGFPGEYANDQERRWTLTAPPGY 40
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 FGNLRSPGWPDNYDNDXDCXVTLTAPQNH 38
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APPLICATION NUMBER: 60/
FILING DATE: 1997-09-12
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FILING DATE: 1997-09-12
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FILING DATE: 1997-08-18
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Young, Peter R
Yue, Tian-Li
                                                                                                                                   USA
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McNulty, Dean E
Rosen, Craig A
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                                                                                                                                                                                                                                                    Smooth Muscle Cell-Derived Migration Factor
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51.7%;
us/08/839,008
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Pred. No.
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Best Local Similarity
"~+~hes 16; Conserv:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
             TELEFAX: 610-270-5090 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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APPLICANT:
                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/563,697
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
SEQUENCE CHARACTERISTICS
                                                            REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
                                                                                                              FILING DATE: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yue, Tian-Li
TITLE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor
NUMBER OF SEQUENCES: 9
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
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                                              TELEPHONE:
                                                                                              NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U:
ZIP: 19406
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STATE: PA
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REGISTRATION NUMBER:
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CLASSIFICATION:
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McNulty, Dean E
Rosen, Craig A
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Young, Peter R
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                                              610-270-5096
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-839-008-7
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                                                                                                                             ; CLONE:
US-09-032-523-8
                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                              Matches
                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FASTSEN: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NITHERIN
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl
APPLICANT: Baugh, Mariah
TITLE OF INVENTION: HUMAN PROTEINASE MOLECULES
NUMBER OF SEQUENCES: 9
                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NERAL INFORMATION:
APPLICANT: Bandma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ent No.
                                                                                                                              MEDILL
LIBRARY: Gell
COME: 2589009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 POR CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
27 PNYTRPVFLCGGDVTGESGYVASEGFPNLYPPNKKCIWTITVPEG 71
                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U. ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 PNYTRPVFLCGGDVTGESGYVASEGFPNLYPPNKKCIWTITVPEG 71
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                          5 PKWPEPVF-----GRLASPGFPGEYANDQERRWTLTAPPG 39
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                                                                Conservative
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                                                                                                                                                                                          linear
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                                                                             31.1%;
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                                                         Score 74; DB 4;
Pred. No. 0.11;
6; Mismatches
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                                                                                          DB 4; Length 468;
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                                                             Indels
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; SOFTWARE: Patent:
; SEQ ID NO 6
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Mouse
US-09-374-135-6
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US-09-374-135-6
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,757
FILING DATE: 10-JUN-1997
CLASSIFICATION 1435
PRIOR APPLICATION UMBER: US/08/609,187
APPLICATION NUMBER: US/08/609,187
APPLICATION NUMBER: US/08/609,187
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-028-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6258584
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/374,135
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/095,982
PRIOR FILING DATE: 1998-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND TITLE OF INVENTION: SECRETED BY PROSTATE AND BLADDER CANCER CELLS FILE REFERENCE: 1703-017.US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1155 Ave
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 GRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 29.0%;
Local Similarity 44.8%;
nes 13; Conservative
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Leong, Kahan
Raitan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Raitano, Arthur B.
Saffran, Douglas C.
Jakobovits, Aya
                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prockop, Darwin J.
Hojima, Yoshio
Li, Shi-Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sieron, Aleksander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROCESSES; METHODS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
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                                                                                                                     ; MOLECULE TYPE: US-08-572-225-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-872-757-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.0%;
best Local Similarity 44.8%;
Matches 13; Conservation
                                                                       Query Match
Best Local Similarity
                                                            Matches
                                                                                                                                                                                                           TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Procko
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/572,225

FILING DATE: 13-DEC-1995
                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ent No.
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
402 GSITSPGWPKEYPPNKNCIWQLVAPTQYR 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600 GSITSPGWPKEYPPNKNCIWQLVAPTQYR 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572-225-1
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TELEPHONE: 415-854-3694
TELEPHONE: 415-854-3694
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CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 GRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                TYPE: amino acid
STRANDEDNESS: un
TOPOLOGY: unknow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 730 amino acids
                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1155 Avenue of the Americas
                                                                                                                                                                                               788 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brenner, Mitch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hojima,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li, Shi-Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                    unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                  protein
                                                                                                                                                                    unknown
                                                                         29.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECOMBINANT C-PROTEINASE AND ITS USE FOR DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Darwin J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                           8389-031
                                                                         Score 69; DB 1
Pred. No. 0.88;
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                                                          Mismatches
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                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                          12;
                                                                                      Length 788;
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                                                          Indels
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                                                         0;
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                                                       Gaps
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                                                         0;
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; LENGTH: 102
; TYPE: PRT
; ORGANISM: Mouse
US-09-374-135-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08991408
Patent No. 6008017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 10; Conserv
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/034,471
FILING DATE: 0.2-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: ATG-500
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/374,135 CURRENT FILING DATE: 1999-08-10 PRIOR APPLICATION NUMBER: 60/095,982 PRIOR FILING DATE: 1998-08-10 NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND
TITLE OF INVENTION: SECRETED BY PROSTATE AND BLADDER CANCER CELLS
FILE REFERENCE: 1703-017.US1
                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ARLETH, ANTHONY J. APPLICANT: WILLETTE, ROBERT N. APPLICANT: ELSHOURBAGY, NABIL A. APPLICANT: LI XIAOTONG TITLE OF INVENTION: HUMAN CARDIA TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
ZIP: 19
                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. BOX 91
CITY: VALLEY FORGE
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 GRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                            APPLICATION NUMBER: US/08/991,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTITSPNWPDKYPSKKECTWAISSTPGHR 29
                                                                                                                                                                                                                                                                                                                                                 19482
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Leong, Kahan
Raitano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raitano, Arthur B.
Saffran, Douglas C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                   USA
610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                              BOX 980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN CARDIAC/BRAIN TOLLOID-LIKE
                                    ATG-50038
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0.12;
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TELEFAX:

610-407-0701

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US-08-872-757-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: HOMO SAPIENS US-09-432-473-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y MOLECULE TYPE: protein
US-08-991-408-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ELSHOURBAGY, NABIL A.
APPLICANT: LI, XIAOTONG
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN
FILE REFERENCE: ATG-50038-D1
CURRENT APPLICATION NUMBER: US/09/432,473
CURRENT FILING DATE: 1999-11-01
EARLIER APPLICATION NUMBER: 08/91,408
EARLIER FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: 08/91
EARLIER APPLICATION NUMBER: 60/034,471
EARLIER FILING DATE: 1997-01-02
                                                                                                                                                                                                                                                                                                   Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4
LENGTH: 591
                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Prockop, Darwin J.

APPLICANT: Hojima, Yoshio

APPLICANT: Li, Shi-Wu

APPLICANT: Sieron, Aleksander

TITLE OF INVENTION: PROCESSES; METHODS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ARLETH, ANTHONY J. APPLICANT: WILLETTE, ROBERT N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               361 GLITSPNWPDKYPSRKECTWEISATPGHR 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hes 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                13 GRLASPGFPGEYANDQERRWTLTAPPGYR 41
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STRANDEDNESS: sir
TOPOLOGY: linear
                                     CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 GRLASPGFPGEYANDQERRWTLTAPPGYR 41
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                   COUNTRY:
                                                                        STREET:
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10036-2711
                                                                                                                                                                                                                                                                                                 Application US/08872757
                                   New York
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                                                                        1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                           Pennie & Edmonds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 5, Application US/08866650 Patent No. 5939321
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Best Local S
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TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CAPPLICANT: CAPPLIC
                                                                                              NAME: Berson, Bennett J
REGISTRAEN NUMBER: 37094
REGISTRAEN NUMBER: 96
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-551-5000
                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: US/08/609,187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
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10; Conserv
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Takahara, Kazuhiko
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Pred. No. 1
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; rrE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-866-650-5
                                                           US-08-991-408-2
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                                                                             RESULT 19
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US-09-021-287-5
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            Sequence 2, Application US/08991408 Patent No. 6008017 GENERAL INFORMATION:
                                                                                                                                                                                    Matches
                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Greenspan, Daniel S
PPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          TELEFAX: 608-251-9166 FORMATION FOR SEQ ID NO:
                                                                                                                        783 GLITSPNWPDKYPSRKECTWEISATPGHR 811
                                                                                                                                                                                                                                                                                                                                                                                       ELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                           LENGTH: 1013 amin
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                  13 GRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 GRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Berson, Bennett
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 South Pinckney Street
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                                                                                                                                                                                                                                                                                                                                                         608-251-9166
ARLETH, ANTHONY J.
                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                             protein
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Pred. No.
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Pred. No.
                                                                                                                                                                                    Mismatches
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-991-408-2
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                                                                                                                                                                                                                                                                                                  US-09-240-473-5
                                                                                                                                                                                                                                                                                                                  RESULT 20
                                                                                                                                                                                                                                                                   Sequence 5, Application US/09240473 Patent No. 6297011
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 11; Conserv
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: AT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                             TITLE OF INVENTION: Mammalian Tolloid-Like Protein NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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TELEFAX: v...
1 ex: 846169
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                                                                                                                                                                                                                                                                                                                                                             783 GLITSPNWPDKYPSRKECTWEISATPGHR 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                  STREET: 1 Sout
CITY: Madison
                                                                                                                      ADDRESSEE: Quaries ... Street
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CITY: VALLEY FORGE
                                                                          ZIP:
                                                                                      COUNTRY:
                                                                                                      STATE:
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ZIP: 19482
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Takahara, Kazuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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LI, XIAOTONG
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PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
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                                           Floppy disk
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37.9%;
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for Windows Version
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                                                                                                                                                                                                                                        Daniel S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
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CURRENT APPLICATION NUMBER: US/09/240,473

FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BESSON, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839

TELEOMNUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEPHONE: 508-251-9166
INFORMATION FOR SEQ UD NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-240-473-5

Y Match
Vy Match
Local Similarity 37.9%; Pred. No. 1.6;

1 : | | : | | : | | : | | | | |
DS GRIASPGFPGEYANDQERRWTLTAPPGYR 41
Db 783 GLITSPNWPDKYPSRKECTWEISATPGHR 811

Search completed: January 11, 2003, 10:54:19

Job time: 68 secs
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Minimum I
Maximum I
                                                                                                                                                                                                                                               Title:
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                                                       number of hits satisfying chosen parameters:
                                                                                                                                         BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                US-09-874-198-1
238
1 TPLGPKWPEPVFGRLASPGF......GEYANDQERRWTLTAPPGYR 41
                                                                                                   283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                           January 11, 2003, 10:44:28; Search time 66 Seconds
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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                           Gapext 0.5
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59.720 Million cell updates/sec
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DB DB seq length: 0 length: 2000000000

Database : PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Maximum Match 100% Listing first 60 summaries

Post-processing: Minimum Match 0%

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

228 98	27	25 5	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	Ġ.			u u	N		Result No.	
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ha ba	hypothetical prote	<u>,                                    </u>	nt subcom	Ţ.	pit.	othetical	Φ,	g	lagen C-	lagen C-	lagen C-		MP-1 lik	₩		procollagen I C-p	UVS.2 protein - A	t subcom	factor-	_	ment subcom	procollagen I C-pr	ebnerin precursor		e fac	Ra-reactive facto	ion	

## ALIGNMENTS

Ra-reactive factor (EC 3.4.21.-) 2 precursor - human RyAlternate names: mannose binding protein-associated serine proteinase 2 (Natternate names: Homo sapiens (Man) C:Species: Homo sapiens (Man) C:Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 16-Jun-2000 C:Accession: A59271 precursor - human
protein-associated serine proteinase 2 (MASP-2)

R:Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, Nature 386, 506-510, 1997
A;Title: A second serine protease associated with mannan-binding lectin that activate A;Reference number: A59271; MUID:97242412; PMID:9087411
A;Accession: A59271

A; Status: nucleic acid sequence not shown; not compared with conceptual translation

A; Molecule type: mRNA A; Residues: 1-686 < JEN>

A;Experimental source: tissue liver
A;Note: submitted to GenBank, December 1996
A;Note: parts of this sequence, including the amino end of the mature protein, C;Genetics: A;Cross-references: GB:Y09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007627

were

A;Gene: GDB:MASP2
A;Cross-references: GDB:6071500
A;Cross-references: GDB:6071500
A;Cross-references: GDB:6071500
A;Map position: lp36.2-lp36.3
C;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement facto C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serin F;1-15/Domain: signal sequence #status predicted <SIC>
F;16-444.445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F;19-134/Domain: Clr/Cls repeat homology <ClRl>
F;142-180/Domain: Clr/Cls repeat homology <ClRl>
F;184-293/Domain: Clr/Cls repeat homology <ClR2>
F;300-361/Domain: Complement factor H repeat homology <FH1>
F;366-430/Domain: complement factor H repeat homology <FH2>
F;366-430/Domain: crypsin homology <TRY>
F;72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-5
F;158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:444-445-Cyleavage site: Arg-Ile (autolytic) #status predicted

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A;Map position: 3q27-3q28
G;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement fac
G;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement fac
G;Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein;
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-448,449-699/Product: Ra-reactive factor #status predicted <MAT>
F;19-135/Domain: Clr/Cls repeat homology <CIR1>
                                                 C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_rev:
C;Accession: T16761
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A;Cross-references: DDBJ:D17525; NID:g439712; PIDN:BAA04477.1; PID:g439713
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Takada, F.; Takayama, Y.; Hatsuse, H.; Kawakami, M. Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A;Title: A new member of the Cls family of complement proteins found A;Reference number: JN0883; MUID:94059062; PMID:8240317
A;Accession: JN0883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
     submitted
                            R; Fulton,
                                                                                                                         hypothetical protein R151.5 - Caenorhabditis elegans
                                                                                                                                                      T16761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Sato, T.; Endo, Y.; Matsushita, M.; Int. Immunol. 6, 665-669, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: MASP1; GDB: CRARF; CRARF1; PRSS5; MASP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ra-reactive
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                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              132/Domain: complement factor H repeat homology <FH1>
143/Domain: complement factor H repeat homology <FH2>
691/Domain: complement factor H repeat homology <FH2>
691/Domain: trypsin homology <TRY>
78,407/Binding site: carbohydrate (Asn) (covalent) #status predicted
-7-91,143-157,153-166,168-181,185-212,242-260,301-349,329-362,367-414,397-432,436-572,
-7-91/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
-448-449/Cleavage site: Arg-Ile (autolytic) #status predicted
-448-449/Cleavage site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comment: This is a serum bactericidal factor that activates complement C4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143-181/Domain: EGF homology <EGF>
185-294/Domain: C1r/C1s repeat homology <C1R2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
Residues: 1-699 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rence number: I54763; MUID:94289349; PMID:801
ssion: I54763
tus: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e: Molecular characterization of a novel serine protease involved in activation rence number: I54763; MUID:94289349; PMID:8018603
                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                    11 VFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                      MFGQIQSPGYPDSYPSDSEVTWNITVPDGFR 57
  to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (man)
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  EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDB:361104; GDB:330954; OMIM:600521
Data
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Library, February 1994
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                                                                                                                                                                                                                                                                                                                                              Pred. No. U.U.
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 238; DB 1;
Pred. No. 4.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-associated
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                                                                     20-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                               .0019;
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                                                                                                                                                                                                                                                                                                                    procollagen I C-proteinase enhancer protein precursor C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text
C;Accession: A55362
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
A55362
                       A; Cross-references: GDB:305468;
                                                 A; Gene: GDB: PCOLCE
                                                                           C; Genetics:
                                                                                               A; Cross-references: GB:L33799;
                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-449 <TAK>
                                                                                                                                                                     A; Status: not compared with
                                                                                                                                                                                               A; Accession: A55362
                                                                                                                                                                                                                       R;Takahara, K; Kessler, E; Bin:
J. Biol. Chem. 269, 26280-26285,
A;Title: Type I procollagen COOH-
A;Reference number: A55362; MUID
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A; Status: preliminary;
A; Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-610 < FUL>
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7q21.3-7q22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rat
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conceptual translation

NID: g642907; PIDN: AAA61949.1; PID: g642908

OMIM:600270

COOH-terminal proteinase enhancer MUID:95014462; PMID:7523404

#text\_change 05-Nov-1999

Eddy, R.L.; Jani-Sait, S.;

protein: identification

human

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R;Li, X.J.; Snyder, S.H.
J. Biol. Chem. 270, 17674-17679, 1995
A;Title: Molecular cloning of Ebnerin, a vc
A;Reference number: A57190; MUID:953535352;
A;Accession: A57190
                                                                                                                                                                                               F:142-245/Domain: scavenger receptor cysteine-rich domain homology <SRC1>F;289-392/Domain: scavenger receptor cysteine-rich domain homology <SRC2>F;583-689/Domain: C1r/C1s repeat homology <C1R1>F;713-816/Domain: scavenger receptor cysteine-rich domain homology <SRC3>F;838-944/Domain: C1r/C1s repeat homology <C1R2>
                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-1290 <LIA>
A;Cross-references: GB.U32681; NID:g975346; PIDN:AAC52248.1;
C;Superfamily: scavenger receptor cysteine-rich domain homolo
                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U32681; NID:g975346; PIDN:ARC52248.1; PID:g975347 C;Superfamily: scavenger receptor cysteine-rich domain homology; Clr/Cls repeat homol C;Reywords: extracellular protein; transmembrane protein protein F:1-77/Domain: scavenger receptor cysteine-rich domain homology #status_atypical <SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Nov-1995 #sequence_revision 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CESP:R151.5
A;Introns: 68/3; 120/1; 151/1; 307/1; 448/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U00036; NID:g458996; A;Experimental source: strain Bristol N2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 RLASPGFPGEYANDQERRWTLTAPPGY 40
GPVWTSPPFVNYTCGGFLTGLSGQFSSPYYPGSYPNNARCLWNIEVPNNYR 875
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                                                                                                  Conservative
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                                                                                                                       35.1%;
31.4%;
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51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid sequence not shown; not compared with conceptual
                                               GRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
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Pred. No. 0.01
5; Mismatches
                                                                                                                          Score 83.5; DB Pred. No. 0.053;
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                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    von Ebner's gland protein
2; PMID:7629065
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0.015;
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                                                                                                                                                  Length 1290;
                                                                                               Indels
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                                                                                                  Gaps
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Biochem. J. 240, 783-787, 1986
A:Title: Cloning and sequencing of full-length cDNA encoding A:Reference number: A29768; MUID:87156625; PMID:3030286
A:Accession: A29768
A:Molecule type: mRNA
A:Residues: I-151, 'L', 153-705 < JOU>
A:Cross-references: GB:X04701; NID:g29538; PIDN:CAA28407.1; PA:Cross-references: GB:X04701; OB:Gagnon, J.
Biochem. J. 241, 711-720, 1987
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F:37-146/Domain: CIr/Cls repeat homology <CIRI>
F:159-270/Domain: CIr/Cls repeat homology <CIRI>
F:159-270/Domain: CIr/Cls repeat homology <CIR2>
F:26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form)
F:26/Modified site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 464-705 <AR2> A; Residues: 464-705 <AR2> R; Thielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; J. Biol. Chem. 265, 14469-14475, 1990 A; Title: Ca(2+) binding properties and Ca(2+)-dependent j. A; Reference number: A37820; MUID:90354439; PMID:2387866 A; Accession: A37820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Arlaud, G.J.; Gagnon, J. Biochemistry 22, 1758-1764, 1983
Biochemistry 22, 1758-1764, 1983
A;Title: Complete amino acid sequence of the catalytic chain of human complement A;Reference number: A00916; MUID:83204782; PMID:6303394
A;Accession: A00916
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                                          A; Molecule type: protein
A; Residues: 18-26; 'L',153-160; 'XX',252-255 <THI>
R; Pelloux, S; Thielens, N.M.; Hudry-Clergeon, G.;
FEBS Lett. 386, 15-20, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 152-186 <AR3>
A; Note: 152-Leu was also i
A; Note: 6.J.; Gagnon, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:TItle: Identification of erythro-beta-hydroxyasparagine in the EGF-like domain A:Reference number: S02422; MUID:88005128; PMID:2820791 A:Accession: S02422
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A; Residues: 1-705 <LEY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: protein sidues: 18-166,'X',168-463 <ARL>
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hud, G.J.; van Dorsselaer
Lett. 222, 129-134, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was also found
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F;464-705/Product: complement CIr chain B #status experimental <BCH>
F;464-705/Product: complement CIr chain B #status experimental <BCH>
F;464-697/Domain: trypsin homology <TRY>
F;71-89,146-165,161-174,176-189,193-220,250-268,309-358,338-371,376-429,406-447,451-5
F;125,221,514,581/Binding site: carbohydrate (Asn) (covalent) #status experimental F;167/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental F;206/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status experime F;463-464/Cleavage site: Arg Ile (autolytic) #status experimental F;502,557,654/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                         C;Superfamily: complement factor H repeat homology F:354-409/Domain: complement factor H repeat homology F:529-886/Domain: complement factor H repeat homology F:707-762/Domain: complement factor H repeat homology F:768-827/Domain: complement factor H repeat homology F:835-892/Domain: complement factor H repeat homology
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A:Title: Cloning and expression of SEZ-6, a brain-specific and seizure-related A;Reference number: I52657; MUID:95240392; PMID:7723619
A;Accession: I52657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: complement subcomponent Clr; Clr/Cls re C;Keywords: acute phase; beta-hydroxyasparagine; calci F;1-17/Domain: signal sequence #status predicted <SIG>F;17-138/Domain: Clr/Cls repeat homology <ClR1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seizure-related protein SEZ-6 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB:D29763; NID:g693909; PIDN:BAA06167.1;
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A; Residues: 1-977 < RES>
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A; Residues: 133-137;187-211;610-613
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Pred. No. 0.055;
                                                                                                                                                                                                        Score 80.5;
Pred. No. 0
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RESULT 8

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A;Cross-references: GB:M18767; NID:g179647; PID
R;Mackinnon, C.M.; Carter, P.E.; Smyth, S.J.; D
Eur. J. Biochem. 169, 547-553, 1987
A;Title: Molecular cloning of cDNA for human co
A;Reference number: S00224; MUID:88082788; PMID
A;Accession: S00224
A;Molecule type: mRNA
A;Residues: 1-688 < MAC>
A;Cross-references: EMBL:X06596; NID:g29542; PI
A;Accession: S26732
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 16-38;68-116;170-236;246-262;265-280;282-284;287-308,315-363;384-394;421-435 R;Tosi, M.; Duponchel, C.; Meo, T.; Couture-Tosi, E. J. Mol. Biol. 208, 709-714, 1989 A;Title: Complement genes Clr and Cls feature an intronless serine protease domain close A;Reference number: S05634; MUID:90040704; PMID:2553984 A;Status: not compared with conceptual translation A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Jun-2002 C;Accession: A40496; A27381; S00224; S26732; S05634; A05140; A25396; A38407; R;Kusumoto, H.; Hirosawa, S.; Salir, J.P.; Hagen, F.S.; Kurachi, K. Proc. Natl. Acad. Sci. U.S.A. 85, 7307-7311, 1988 A;Title: Human genes for complement components Clr and Cls in a close tail-to A;Reference number: A40496; MUID:89017187; PMID:2459702
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999
C;Accession: T09456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement subcomponent C 1SBAR.GIF (EC 3.4.21.42) precursor N;Alternate names: C1 esterase precursor C:Species: Homo sapiens (man)
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Residues: 1-688 <TOS>
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Residues: 1-688 <KU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i, M.; Duponchel, C.; Meo, Cemistry 26, 8516-8524, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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15; Conserv
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PMID:3500856
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В

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YAEPTMYGEILSPNYPQAYPSEVEKSWDIEVPEGY

RESULT

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A; Note: the list of introns may be incomplete
C; Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement
C; Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement
F; 1-15/Domain: signal sequence #status predicted <SIG>
F; 11-127/Domain: Clr/Cls repeat homology <ClRl>
F; 16-688/product: complement subcomponent Cls #status experimental <MAT>
F; 16-437/Product: complement subcomponent Cls #status experimental <MAT>
F; 135-171/Domain: EGF homology <EGF>
F; 135-171/Domain: Clr/Cls repeat homology <ClRl>
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A;Residues: 131-134, 'X',136-146, 'X',148-150;155, 'X',157-162;166-170, 'X',172-174, 'X',1
A;Residues: 131-134, 'X',136-424, 'X',426-431;547-556;592-597;617, 'X',619-627, 'X',629-
R;Thielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.
J. Biol. Chem. 265, 14469-14475, 1990
A;Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated A;Reference number: A37820; MUID:90354439; PMID:2387866
A;Accession: B37820
                                                                                                                                                                                                            F;438-688/Product: complement subcomponent C1s chain B (light chain) #status experime F;438-675/Domain: trypsin homology <TRY> F;65-83,135-147,143-155,158-171,175-202,234-251,294-341,321-354,359-403,386-421,425-5 F;149/Modified site: erythro-beta-hydroxyasparagine (Asn) (partial) #status experimen F;174,406/Binding site: carbohydrate (Asn) (covalent) #status experimental F;437-438/Cleavage site: Arg-Ile (complement subcomponent C1r) #status experimental F;437-438/Cleavage site: Arg-Ile (complement subcomponent C1r) #status experimental
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A;Molecule type: protein
A;Residues: 16-25;'X',203-207 <THI>
A;Residues: 16-25;'X',203-207 <THI>
A;Residues: N.M.; Van Dorsselaer
A;Thielens, N.M.; Van Dorsselaer
Biochemistry 29, 3570-3578, 1990
A;Title: Chemical and functional characterization of a fragment of C1s
A;Reference number: A32672; MUID:90283368; PMID:2141278
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A; Residues: 16-61;168-219;287-293,'K',295-334;384-445 <S
R; Hess, D.; Schaller, J.; Rickli, E.E.
Biochemistry 30, 2827-2833, 1991
A; Title: Identification of the disulfide bonds of human
A; Reference number: A38407; MUID:91175725; PMID:2007122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Contents: annotation; erythro-beta-hydroxyasparagine site, content A;Note: about half of the A chains contain erythro-beta-hydroxyasparagine C;Comment: This protein is a serine proteinase that combines with Clq and
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;294-354/Domain: complement factor H repeat homology <FH1>F;359-421/Domain: complement factor H repeat homology <FH2>
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A;Title: The serine proteinase chain of human complement component Cls. Cyanogen brom A;Reference number: A05140; MUID:84104122; PMID:6362661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 291/1;
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A; Residues: 438-483, 'X', 485-500; 503-534; 542-558; 561-572, 'A', 574-601; 617-623; 626-644; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comment: Cls is a dimer
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       7 WPEP-VFGRLASPGFPGEYANDQERRWTLTAPPGY 40
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                                                                                                                   Similarity
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                                                                                                                   31.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of identical chains, each of
                                                                                                               Score 74.5; DE Pred. No. 0.33;
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0; PMID:3007145
                                                                                                                                                    DB
                                                                              13;
                                                                                                                                                 Length
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N;Alternate names: p14 protein
C;Species: Mus musculus (house mouse)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 05-Nov-1999
C;Accession: JH0403
R;Lecain, E.; Zelenika, D.; Laine, M.C.; Rhyner, T.; Pessac, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-319 <SAT>
A; Cross-references: GB:M27162; NID:g214871; PIDN:AAA49980.1; PID:g214872
C; Superfamily: astacin homology
C; Keywords: zinc
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Apr-2001
C;Accession: I51569
R;Sato, S.M.; Sargent, T.D.
Dev. Biol. 137, 135-141, 1990
                                                C:Date: 10-Sep-1999 #sequence_revision 10-Sep C:Accession: S05008 R:Kinoshita, H: Sakiyama, H: Tokunaga, K: FEBS Lett. 250, 411-415, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Neurochem. 56, 2133-2138, 1991
A:Title: Isolation of a novel cDNA corresponding to a transcript A:Reference number: JH0403; MUID:91225708; PMID:2027019
A:Accession: JH0403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Biol. 137, 135-141, 1990
A;Title: Molecular approach to dorsoanterior development A;Reference number: I51569; MUID:90108413; PMID:1688538 A;Accession: I51569
FEBS Lett. 250, 411-415, 1989
A;Title: Complete primary structure of a calcium-dependent serine proteinase A; Reference number: S05008; MUID:89325606; PMID:2753140
A;Accession: S05008
                                                                                                                          complement
C; Species:
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A; Residues: 1-402 <LEC>
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                                                                                                                                                                                                                                                                                                                                                                           /Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                   PNYTRPVFLCGGDVTGESGYVASEGFPNLYPPNKKCIWTITVPEG
                                                                                                                         subcomponent C 1SBAR.GIF (EC 3.4.21.42) precursor Mesocricetus auratus (golden hamster)
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Pred. No. 0.17;
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                                                                    Imajoh-Ohmi,
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                                                                                                      #text_change
                                                                                                                                                                                                                                                                                                                                       Length 402;
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A;Cross-references: EMBL:X16160; NID:g49621; PIDN:CAA34286.1; PID:g49622
A;Note: part of this sequence, including the amino ends of both the heavy and light c
C;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement facto
C;Reywords: beta-hydroxyasparagine; calcium binding; duplication; glycoprotein; hydro
F;12-1Domain: signal sequence #status predicted <SIG>
F;11-13J/Domain: Clr/Cls repeat homology <CIR1>
F;22-444/Product: serine proteinase heavy chain #status experimental <HCH>
F;141-177/Domain: EGF homology <EGF>
F;181-29J/Domain: Complement factor H repeat homology <FH1>
F;300-360/Domain: complement factor H repeat homology <FH2>
F;445-682/Domain: crypsin homology <TRY>
F;445-682/Domain: trypsin homology <TRY>
F;445-682/Domain: trypsin homology <TRY>
F;441-153,149-162,164-177,181-208,240-257,300-347,327-360,365-410,392-428,432-5
F;155/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;180,433/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                           tolloid-BMP-1 like protein 1 - California sea hare %,Alternate names: probable metalloprotease TBL-1 C:Species: Aplysia californica (California sea hare) C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #:C:Accession: T31069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; J. Biol. Chem. 273, 5235-5242, 1998
A;Title: The intrinsic factor-vitamin B12 receptor and target of A;Reference number: Z16459; MUID:98148073; PMID:9478979
A;Accession: T08618
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999
A; Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by A; Reference number: 220965; MUID:98007484; PMID:8987797
                                                        R;Liu, Q.R.; Hattar, S.; Endo, J. Neurosci. 17, 755-764, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F; 133-164/Domain: F; 436-467/Domain:
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A; Residues: 1-3623 < M
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nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL:AF022247; NID:g3834379; PIDN:AAC71661.1; PID:g3834380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.5%;
                                                                                S.; MacPhee, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
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7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 72;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                             Zhang, H.;
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                                                                                                                                         #text_change 18-Aug-2000
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                                                                                Cleary, L.J.;
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A; Gene: GDB:BMP1
A; Cross-reference
A; Map position: 8
C; Function:
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                                                                                                                                            procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - hums N;Alternate names: bone morphogenic protein splice form BMP-1/His C;Species: Homo sapiens (man) C;Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999 C;Accession: A37278; A58788 R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kr. Science 242, 1528-1534, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen ty C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; F;1-22/Domain: signal sequence #status predicted <SIG>
A;Title: Novel regulators of bone formation: molecular clones A;Reference number: A37278; MUID:89072730; PMID:3201241 A;Accession: A37278 A;Accession: A37278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;1-22/Domain: signal sequence #status predicted <SIG>;23-73/Domain: signal sequence #status predicted <MAT>;23-73/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>;130-321/Domain: astacin homology <AST>;32-431/Domain: C1r/C1s repeat homology <C1R1>;435-431/Domain: C1r/C1s repeat homology <C1R2>;551-587/Domain: EGF homology <CGF>;551-700/Domain: C1r/C1s repeat homology <C1R3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted 163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
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Residues: 1-730 <WOZ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1;
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ession: A37278; E58788
zney, J.M.; Rosen, V.; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,217,223,272/Binding site: zinc (His, His, His, Tyr) #status
/Active site: Glu #status predicted
/Modified site: erythro-beta-hydroxyasparagine (Asn) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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39.5%;
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Pred. No. 1
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                                                                                                                                                                                             R.W.;
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F:33-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <APP = 130-321/Domain: astacin homology <ASTP = 132-431/Domain: Clr/Cls repeat homology <ClR1> = 132-431/Domain: Clr/Cls repeat homology <ClR2> = 1551-587/Domain: Clr/Cls repeat homology <ClR2> = 1551-587/Domain: Clr/Cls repeat homology <ClR3> = 1591-700/Domain: Clr/Cls repeat homology <ClR2> = 1591-700/Domain: Clr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;214/Active site: GIU #Status previews
F;565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen C; Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homolog C; Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication C; Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication E;1-22/Domain: signal sequence #status predicted <SIG>
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A;Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld)
A;Reference number: A58788; MUID:95096114; PMID:7798260
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C; Function:
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J. Biol. Chem. 269, 32572-32578, 1994
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A;Map position: 8p21-8p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB:BMP1; BMP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 703-823 <TAK>
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     3.4.24.19) precursor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 69; DB 1;
Pred. No. 1.9;
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     tolloid-like
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A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen C;Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homolog C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplicatior E;1-22/Domain: signal sequence #status predicted <SIG>
                                                                                                                           A;Cross-references: GDB:125203; OMIM:112264
A;Map position: 8p21-8p21
C;Function:
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                                                                                                                                                                                                                                                                                           A; Residues: 703-986 <TAK>
A; Cross-references: GB:L35279;
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A; Residues: 703-986
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A; Residues: 1-702, 'EKRPALQPPRGRPHQLKFRVQKRNRTPQ'
A; Cross-references: GB.M22488; NID:9179499; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: bone morphogenic protein 1, tolloid-like splice form
C;Species: Homo sapiens (man)
C;Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are A; Reference number: A58788; MUID:95096114; PMID:7798260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Novel regulators of bone formation: molecular clones and activities A; Reference number: A37278; MUID:89072730; PMID:3201241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Wozney, J.M.; Rosen, V.; Co
Science 242, 1528-1534, 1988
                                                                                                                                                                                                                           A; Gene: GDB: BMP1; BMP-1
                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: B58788
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A58788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 269, 32572-32578, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A37278
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                                                                                                                                                                                                                                                                Genetics:
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                                                                                                                                                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz,
                                                                                                                                                                                                                                                                                           NID: g619860; PIDN: AAC41710.1;
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PIDN:AAA51833.1;
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C;Species: Drosophila melanogaster
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C;Accession: S58984
R;Finelli, A.L.; Xie, T.; Bossie, C.A.; Blackman, R.K.; Padgett, R.W.
Genetics 141, 271-281, 1995
A;Title: The tolkin gene is a tolloid/BMP-1 homologue that is essential for A;Reference number: S58984; MUID:96042912; PMID:8536976
A;Accession: S58984
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F:707-742/Domain: EGF homology <EG29-
F:747-856/Domain: CIr/CIs repeat homology <CIR4>
F:747-856/Domain: CIr/CIs repeat homology <CIR5>
F:860-973/Domain: CIr/CIs repeat homology <CIR5>
F:91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:11,142,332,363,599/Binding site: carbohydrate (Asn) (597-572,574-587,591-617,644-66
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,717,223,2772/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214,Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                  RESULT 19
S58984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I49540
       A; Molecule type: mRNA
A; Residues: 1-1464 <FIN>
A; Cross-references: EMBL
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A; Residues: 1-991 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Embryonic expression of mouse bone morphogenetic A; Reference number: I49540; MUID:94229342; PMID:8174772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Fukagawa, M.; Noboru, : Dev. Biol. 163, 175-183,
                                                                                                                                                                                                                                                                                  development protein tolkin (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: Bmp-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: procollagen C-endopeptidase; astacin Keywords: hydrolase; metalloproteinase; zinc 135-336/Domain: astacin homology <AST> 556-592/Domain: EGF homology <EG1>
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Best Local
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435-544/Domain: Clr/Cls repeat homology <ClR2>
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130-321/Domain:
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12-747/Domain: ECF homology <EG2>
222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
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EMBL: U34777; NID: g1002985; PIDN: AAC47015.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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2.3;
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2.3;
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  PID: g1002986
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A; Note: the aut C; Genetics:
A; Gene: tolkin
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C;Superfamily: astacin homology; EGF homology
C;Keywords: hydrolase; metalloproteinase; zinc
F;529-722/Domain: astacin homology <AST>
F;958-993/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                            R:Nunes, D.P.; Keates, A.C.; Afdhal, N.H.; Offner, G.D. Blochem. J. 310, 41-48, 1995
A;Title: Bovine gall-bladder mucin contains two distinct A;Reference number: S56744; MUID:95374471; PMID:7648470
A;Accession: S56745
                                                                                                                                                                                                                 #;Cross-references: GB:S78869; NID:g1042038; PIDN:AAB35070.1; PID:g1042039
C;Superfamily: C1r/C1s repeat homology; scavenger receptor cysteine-rich dd
F;197-305;Domain: C1r/C1s repeat homology <C1R2>
F;311-417/Domain: scavenger receptor cysteine-rich domain homology <SRC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
Search completed: January Job time : 69 secs
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A; Residues: 1-504 < NU
                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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12; Conserv
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Pred. No. 1
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Pred. No. 3
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1: sp_archea:*
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sp_bacteriap:*
sp_archeap:*
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Ogaxa4 mus musculu
Ogaxd5 mus musculu
Ogaxd2 mus musculu
Ogaxd2 mus musculu
Ogaxd38 mus musculu
Ogaxd4 rattus norv
Ogaxd4 rattus norv
Ogaxd5 rattus norv
Ogax8 rattus norv
                                                                                                                                               Q9umv3 homo sapien
Q9ulc7 homo sapien
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7620 3620 421 707 707 707 707 1139 228 623 3623 3623 414 414 414 685 685 685 685 685 735 735 735 735 735 735 735 735 735 73	728 933 96 3138 1280 1290 719 719 977 997 991 1048 3560 3560 3560
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099sz5 099t153 089002 089002 099t60 099670 099670 09944w1 09944w2 090244 09cx06	Q96rs4 Q9d2080 Q9d2080 Q9d248 Q9uct48 Q9uct90 Q9vtp0 Q92872 Q62287 Q62224 Q6223 Q623 Q6

## ALIGNMENTS

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Matches 41
Query Match
Best Local Similarity
                                                                                            SMART; SM00042; CUB; 1.

SMART; SM000179; EGF_CA; 1.

PROSITE; PS00010; ASX_HYDROXYL; UNK)

PROSITE; PS01180; CUB; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 1.

Calcium-binding; EGF-like domain; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9ULC7;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                               Takahashi M., Fujita T.;

Partial genomic structure of human MBL-associated serine |

MASP)-2 (from exon 1 to exon 5).";

Submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 CUB DOMAIN.

EMBL; AB033742; BAA85659.1; -.

EMBL; AB033742; BAA85659.1; -.
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InterPro;
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PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
Calcium-binding; EGF-like domain;
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Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MBL-associated
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SM00179; EGF_CA; 1.
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IPR000859; CUB_domain.
IPR000561; EGF-like.
IPR001881; EGF_Ca.
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IPR000859; CUB_domain.
IPR000561; EGF-like.
IPR001881; EGF_Ca.
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1. 13, Last sequence update)
1. 21, Last annotation update)
protease(MASP)-2 (Fragment).
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MANNOSE BINDING
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Score 238; DB 4;
Pred. No. 3.2e-23;
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No. 3.1e-23;
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                     Length 181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB008047; BAA78616.1; -.
EMBL; AB03742; BAA85658.1; -.
EMBL; Y18281; CAB50728.1; -.
EMBL; Y18283; CAB50730.1; -.
EMBL; Y18286; CAB50730.1; -.
EMBL; Y18287; CAB50734.1; -.
EMBL; Y18287; CAB50734.1; -.
EMBL; AF321558; AAC50275.1; -.
HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UBP3;
Q9UBP3;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB-LIVEK;
MEDLINE-99192764; PubMed=10092804;
Stover C.M., Thiel S., Thelen M., Lynch N.J.
Jensenius J.C., Schwaeble W.J.;
"Two constituents of the initiation complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99262288; PubMed=10330290; Takahashi M., Endo Y., Fujita T., Matsushita M.; Matsushita M.; Takahashi M., Matsushita M.; Matsushi
                             PROSITE; PS00100; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGE_2; 1.
PROSITE; PS01187; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure of Human WASP-2 Gene.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL; Y18284; CAB50731.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takahashi M., Fujita T.;
"Partial genomic structure of human
(MASP)-2 (from exon 1 to exon 5).";
Submitted (OCT-1999) to the EMBL/Ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAP19 (19 kDa) precursor (19 kDa) MASP-2 OR SMAP OR MASP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TYEMBLEE. 13, Last sequence update) 01-JUN-2002 (TYEMBLEE. 21, Last annotation update) Mannose binding lectin-associated serine protease-2 related protein, MAP19 (19 kDa) precursor (19 kDa) (MBL-associated protein MAP19).
Calcium-binding; EGF-like domain; Glycoprotein; Lectin; Protease;
                                                                                                                                                                                SMART; SM00042; CUB; 1.
SMART; SM00179; EGF_CA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              structural gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; S01.229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Park D., Kim B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR
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                                                                                                                                                                                                                                                       PF00431; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                          IPRO00152; Asx_hydroxyl.
IPRO00859; CUB_domain.
IPRO00561; EGF-like.
IPRO01881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11:859-863(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baek K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yoon J.;
-2 Gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MBL-associated serine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the mannose-binding encoded by a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases
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RESULT
Q9QXD5
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Best Local S
Matches 32
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Best Local S
Matches 41
                                                                                                                                                                                                  990XA4 PRELIMINARY;
990XA4;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
Mouse MAP19 precursor.
MASP2 OR MASP-2/MAP19.
          09QXD5;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                           MGD; MGI:1330832; Masp2.
InterPro; IPR000152; Asx.hydroxyl.
InterPro; IPR000559; CUB_domain.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=20054576; PubMed=10586086;

MEDLINE=20054576; PubMed=10586086;

Stover C.M., Thiel S., Lynch N.J., Schwaeble W.J.;

The rat and mouse homologues of MASP-2 and MApl9, components mannan-binding lectin activation pathway of complement.";

J. Immunol. 163:6848-6859(1999).

-1-SIMILARITY: CONTAINS 1 CUB DOMAIN.

EMBL; AJ250369; CAB63701.1; -

HSSP; P00736; 1APO.

MESSP; P00736; 1APO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                   SEQUENCE
                                                    Q9QXD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                              1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                 TLLGSKWPEPVFGRLVSPGFPEKYADHQDRSWTLTAPPGYR 56
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                                                                                                                                                     Similarity
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  binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                                                                                                   185 AA;
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           (TrEMBLrel.
                                                                                                                                            Conservative
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                                                   PRELIMINARY;
                               (TrEMBLrel.
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16
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  lectin-associated
                                                                                                                                                                                185 M
; 20973 MW;
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Rodentia;
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78.0%;
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13,
21,
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                                                                                                                                         Score 183; DB Pred. No. 4.7e 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation
                                                                                                                                                                                 MOUSE MAP19.
; 72E01900D30A18B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (19
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MANNOSE BINDING LECTIN-ASSOCIATED PROTEASE-2 RELATED PROTEIN, MAP19
                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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serine protease-2
                                                                                                                                                                                                              Glycoprotein; Repeat; Signal
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No. 3.3e-23;
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                                                   190
                                                                                                                                                    4.7e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
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                                                                                                                                                             DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae;
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                                                                                                                                                            Length 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murinae;
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RESULT
Q9QXD2
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Best Local :
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Q9QXD2;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2002
                                                       pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM000179; EGF_CA; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01181; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
Calcium-binding; EGF-11ke domain; Glycoprotein; Lectin; Protease;
MGD; MGI:1330832; Masp2.
InterPro; IPR000152; Asx_hydrox; InterPro; IPR000859; CUB_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-ZUVOTATO, SCHWaeule Stover C.M., Thiel S., Lynch N.J., Schwaeule Stover C.M., Thiel S., Lynch N.J., Schwaeule The rat and mouse homologues of MASP-2 and The rat and mouse homologues of MASP-2 and The rational Parties of Mase and The rational Parties of The Research Parties of The Resea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-C57BL/6 X CBA;
MEDLINE-20054576; PubMed-10586086;
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                            MEDLINE=20054576; PubMed=10586086;
                                                                                                                                                                                                                                                                                   STRAIN-B6CBAF1/J;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Immunol. 163:6848-6859(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mannan-binding lectin activation pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090; [1]
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                           MASP2 OR MASP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mannose binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAP19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLLGSKWPEPVFGRLVSPGFPEKYADHQDRSWTLTAPPGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y19160; CAB65247.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                          S (Mouse).

Metazoa; Chordata; C

Metazia; Rodentia; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            lectin-associated serine protease-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 F
21457 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.98;
78.08;
                    Asx_hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 183; DB
Pred. No. 4.9e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22BC6BA3F906B010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schwaeble W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9e-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 components ment.";
                                                                                                                                                                                                      components ment.";
                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT Q92338 ID Q92338 ID Q92338 AC Q9 DT Q9 DT
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                                                                                                                                                                                                                         HSSP; P007b3, ...

MESOPS; S01.229; ...

MED; MGI:1330832; Masp2.

(InterPro; IPR000152; Asx_hydroxyl.

R InterPro; IPR0001314; Chymotrypsin.

TherPro; IPR000859; CUB_domain.

TherPro; IPR000859; CUB_domain.
                                                                                                                                                                                                                                                                                                                                                                                              TRYPSIN FAMILY.
EMBL; AB009459; BAA34674.1;
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Mannose-binding lectin associated serine protease-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00431; CUB; 2.
Pfam; PF00084; SuShi; 1.
PRINTS; PR00277; INSULINB.
SMART; SM00032; CCD; 1.
SMART; SM00042; CUB; 2.
SMART; SM00179; EGF_CA; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
SMART; SM00032; CCP; 2.
SMART; SM00042; CUB; 2.
SMART; SM00179; EGF_CA;
SMART; SM00020; Tryp_SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01180; CUB; 2.
PROSITE; PS01186; EGF_Z; 1.
PROSITE; PS01187; EGF_CA; 1.
Calcium-binding; EGF-like domain; Glycoprotein; Lectin; Protease;
                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endo Y., Takahashi M., Nakao M.,
Nonaka M., Fujita T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALB/C; TISSUE=LIVER;
MEDLINE=99008558; PubMed=9794427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9Z338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9Z338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                             PRINTS; PR00722;
                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MASP2 OR MASP-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004825; InterPro; IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Two lineages of mannose-binding lectin-associated MASP) in vertebrates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 TLLGSKWPEPVFGRLVSPGFPEKYADHQDRSWTLTAPPGYR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunol. 161:4924-4930(1998).
- SIMILARITY: CONTAINS 2 CUB DOMAINS.
- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                          PF00084; sushi; 2.
PF00089; trypsin; 1.
S; PR00722; CHYMOTRYPSIN
                                                                                                                                                             PF00431; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Similarity 32; Conser
                                                                                                                                                                                                        IPR000561; I
IPR001881; I
IPR001254;
                                                                                                                                                                                     IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000561;
IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367
367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 P
367
; 40950 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF-like.
EGF_Ca.
Ins/IGF/relax.
Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.9%;
78.0%;
                                                                                                                                                                                   Ser_protease_Try.
Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 183;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F66FCB29CEAB2B7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saiga H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       685
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.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sekine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsushita M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease
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RESULT
Q9JJS8
ID Q9
AC Q9
DT 01
DT 01
DT 01
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Q91WP0
ID Q9
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Best Local S
Matches 32
                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01040; TRYPSIN_DOM; 1.
PROSITE; PS001040; TRYPSIN_SER; 1.
Calcium-binding; EGF-like domain; Glycoprote; Protease; Repeat; Serine protease.
SEQUENCE 685 AA; 75490 MW; 4571E1AE0703A;
Q9JJS8
Q9JJS8;
Q1-OCT-2000
Q1-OCT-2000
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    091WPO:

01-DEC-2001 (TrEMBLrel. 19, Created)

01-DEC-2001 (TrEMBLrel. 19, Last sequenc

01-JUN-2002 (TrEMBLrel. 21, Last annotat

Similar to mannan-binding lectin serine
                                                                                                                                                                                                                      PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS01187; EGF_CA; UNKNOWN_1.
PROSITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; C
                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                        Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                  Pfam; PF00084; sushi; 2.
                                                                                                                                                                                                                                                                                                                               Pfam; PF00431; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.229;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q91WP0
                                                                                                                                                                                                             нydrolase;
                                                                                                                                                                                                                                                                                              SMART; SM00181; EGF;
                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                        16
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                                                                                                                              Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                    TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                       TLLGSKWPEPVFGRLVSPGFPEKYADHQDRSWTLTAPPGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLLGSKWPEPVFGRLVSPGFPEKYADHQDRSWTLTAPPGYR
                                                                                                                                                                                                                                                                                                                                                                                                                          tted (SEP-2001) to the EMBL/GenBank/DDBJ databases BC013893; \mbox{AAH13893.1};\ \mbox{-}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32; Conservative
                                                                                                                                                                                                                                                                                                                            IPROVIEST: EGF_Ca.
IPRO01254: Ser_protease_Try.
TOBO00436: Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                      IPR000152;
IPR000859;
                                                                                                                                                                                                                                                                                                                                                              IPR000859; CUB_domain.
IPR000561; EGF-like.
IPR001881; EGF_Ca.
                                                                                                                                                                                                   685
                                                                                                                                                                                                              Lectin;
                                                                                                                                                     Conservative
                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                   ΑĄ;
                                                                                                                                                                                                  Protease; Serine
75516 MW; F56A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                76.9%;
78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.9%;
78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                   Asx_hydroxyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 183; Pred. No. 2.2e-3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation updat
                                                                                                                                                                Score 183; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                  erine protease.
F56A6D522BC7099D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4571E1AE0703A70F CRC64;
                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protease
                                                                                                                                                                DB 11;
.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
.2e-15;
                                               AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
otease 2
                                                                                                                                                     6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56
                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                            685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lectin;
                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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) (TrEMBLrel.) (TrEMBLrel.)

15, 15, 21,

Last sequence update)
Last annotation update)

Created)

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RESULT
Q9QXD4
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                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00431; CUB; 2.

Pfam; PF00089; sushi; 2.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00032; CCP; 2.

SMART; SM00042; CUB; 2.

SMART; SM00042; Tryp_SPc; 1.

SMART; SM00020; Tryp_SPc; 1.

SMART; SM00010; ASX_HYDROXYL; UNK)

PROSITE; PS01180; CUB; 2.

PROSITE; PS01187; EGF_C; 1.

Calclum-binding; EGF_1; EGF_C; 1.

Calclum-binding; EGF_1; EGF_C; 1.

Calclum-binding; EGF_1; EGF_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-like.
InterPro; IPR001861; EGF-Ca.
InterPro; IPR001254; Ser_protease_Ti
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                           01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                         SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteases: Effects of naturally occuring. Biol. Chem. 275:30962-30969(2000).
-!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-!- SIMILARITY: BELONGS TO PEPTIDASE F/
                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ277747; CAB90832.1; HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                          Q9QXD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Interaction of mannose-binding protein voroteases: Effects of naturally occuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20469449; PubMed-10913141;
SEQUENCE
                                                         Rattus norvegicus (Rat).
                                                                     MASP-2.
                                                                                  MASP-2
                                                                                                                                                                                                                                                                           ry Match
                                                                                                                                                                                                                                                                                                                                                            Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MASP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mannose-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EROPS; S01.229;
                                                                                                                                                                                                                                                                                                 EQUENCE
                                                                                                                                                                  10
                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                      9
                                                                                                                                                                                                                         1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRYPSIN FAMILY
                                                                                                                                                                                                    TLLGSKWPEPVFGRLVSPGFPEKYGNHQDRSWTLTAPPGFR 49
                                                                               protein
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                            Serine
FROM N.A
                                                                                         0 (TrEMBLrel.
0 (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dodd R.B.;
                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                         13 4
                                                                                                                                                                                                                                                                                                   AA:
                                                                               precursor.
                                                                                                                                                                                                                                                                                                                                                           protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                74734 MW;
                                                                                                                                                                                                                                                             75.6%;
75.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sushi_SCR_CCP
                                                                                         13,
13,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated
                                                                                                                                                                                                                                                                                                                                                            Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .•
                                                                                                                 Created)
                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                  Score 180; DB
Pred. No. 5.3e
3; Mismatches
                                                                                                                                                                                                                                                                                                             MANNOSE-BINDING PROTEASE-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Veri
Sciurognathi;
                               Craniata; Ver
Sciurognathi;
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                 16680E4A9ADCCC05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serine protease-2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAMILY
                                                                                                                                          186
                                Vertebrata;
thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata;
                                                                                                                                                                                                                                                             DB 11;
5.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with associated
mutations.";
                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S1;
                                                                                                                                                                                                                                                                                                                       PROTEIN ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALSO
                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
; Murinae; Rattus.
                                            Euteleostomi;
                                 Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNOWN
                                                                                                                                                                                                                                                                          678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AS
                                                                                                                                                                                                                                                                                                                                                                      Protease,
                                                                                                                                                                                                                                                  0
                                 Rattus
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                        SERINE
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RESULT
Q9QX86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          090x86
090x86;
01-MAY-2000
01-MAY-2000
01-JUN-2002
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SMART; SM00179; EGF_CA; 1.

PROSITE; PS00100; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 1.

Calcium-binding; EGF-like domain; Glycoprotein; Repeat; Calcium-binding; CGF-like domain; C
                                                                                                           SMART; SM00042; CUB; 1.
SMART; SM00179; EGF_CA; 1.
PROSITE; PS00100; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF_CA; 1.
Calcium-binding; EGF_like domain; Glycopro
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000152; Asx_hydroxyl
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR001881; EGF_Ca.
Pfam; PF00431; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-FISHER 344;
MEDLINE-20054576; PubMed-10586086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mannan-binding lectin activation pathway J. Immunol. 163:6848-6859(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stover C.M., Thiel S., Lynch N.J., Schwaeble W.J.; "The rat and mouse homologues of MASP-2 and MAp19, compmannan-binding lectin activation pathway of complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y18570; CAB65387.1; HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y19161; CAB65248.1; -. HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=WISTAR; MEDLINE=20054576; PubMed=10586086;
                                   CHAIN
                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAP19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 1 CUB DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000152; Asx_hydroxyl.
IPR000859; CUB_domain.
IPR000561; EGF-like.
IPR001881; EGF_Ca.
      177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 AA; 21053 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last seq
(TrEMBLrel. 21, Last annuln precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                   <u>ہ</u> ۵
   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.4%;
73.2%;
   20113
   ΜW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 170; DB 11;
Pred. No. 2.4e-14;
3; Mismatches 8
POTENTIAL.
92F3CDCA5A1AD489 CRC64;
                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30878EACB604C374 CRC64;
                                                                                                                           Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41
                                                                                                                        Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       components ment.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                components
                                                                                                                     Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
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RP SI
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Q9QX88
                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEPERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam; pF00043; CUB; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00179; EGF_CA; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF_C; 1.
PROSITE; PS01186; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
SIGNAL

15
POTENTIAL.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9QX88;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                           Q9QX83 PRELIMINARY; PRT; 216 AA. Q9QX83; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) MASP-2 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20054576; PubMed=10586086; Stover C.M., Thiel S., Lynch N.J., Schwaeble W.J.; "The rat and mouse homologues of MASP-2 and MAp19, components mannan-binding lectin activation pathway of complement."; J. Immunol. 163:6848-6859(1999).
                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                             MASP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-Like.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-FISHER 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9QX88
     SEQUÉNCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match
                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLLGSKWPEPVFGRLVSLAFPEKYGNHQDRSWTLTAPPGFR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y18568; CAB65385.1; -. P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 68.9%;
Similarity 70.7%;
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
     N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor
                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21010 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.9%;
70.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13,
13,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUB DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 164; DB
; Pred. No. 1.4e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 164; DB
Pred. No. 1.3e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                          Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF22111364C5140C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185
                                                                                                   Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
l.4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
l.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                             Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                             Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ō,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
DDR RET DDR REAL DDR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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RESULT
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Best Local S
Matches 29
                                                                                                                                                                                                                                                                                                                                                 Q9PVY4 PRELIMINAKY; FALL
Q9PVY4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
InterPro;
                                                                                                                                                                                                                     Endo
                                                                                                                                                                                                                                                                                                          PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
CTOCCUM-binding; EGF-like domain; Glycopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00277; INSULINB.
SMART; SM00042; CUB; 1.
SMART; SM00179; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB009072; BAA
HSSP; P00763; 1DPO.
                                                                                                                                     J. Immunol. 161:4924-4930(1998).
-!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                        Nonaka M., Fujita T.; "Two lineages of mannose-binding
                                                                                                                                                                                                                                                                                  Xenopodinae; Xer
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y18573; CAB65390.1; HSSP; P00736; 1APQ.
                                                                                 MEROPS; S01.229;
                                                                                                                                                                                                                                  MEDLINE=99008558; PubMed=9794427;
                                                                                                                                                                                                                                                TISSUE=LIVER;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                  InterPro;
                             InterPro;
                                           InterPro;
                                                       InterPro;
                                                                     InterPro;
                                                                                                                                                                             (MASP) in vertebrates."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20054576; PubMed=10586086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=FISHER 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                          TRYPSIN FAMILY
                                                                                                                                                                                                                   Y., Takahashi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLLGSKWPEPVFGRLVSLAFPEKYGNHQDRSWTLTAPPGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00431; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
               ; IPR000152; Asx_hydroxyl.

; IPR001314; Chymotrypsin.

; IPR000859; CUB_domain.

; IPR000561; EGF-like.

; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000152: Asx_hydroxyl.
IPR000859; CUB_domain.
IPR000561; EGF-like.
    IPR001254;
                                                                    IPR000152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216
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216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                  xenopus
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                                                                                                             BAA86865.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
>216
216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24359 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.9%;
70.7%;
Ser_protease_Try.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF_Ca
                                                                                                                                                                                                                   Nakao M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nain; Glycoprotein;
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A57781AA99B8390C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                    Saiga H.,
                                                                                                                                                                                           lectin-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
.7e-13;
                                                                                                                                                                                                                    Sekine H.,
                                                                                                                                        S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
                                                                                                                                        ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  components of the
                                                                                                                                                                                           serine
                                                                                                                                        KNOWN
                                                                                                                                                                                                                     Matsushita M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal
                                                                                                                                                                                           protease
                                                                                                                                        AS
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InterPro;

IPR000436;

Sushi\_SCR\_CCP

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RESULT
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                                                        RRA PROCCOCE DIT
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R Pfam; PF00008; EGF; 1.

R Pfam; PF00008; trypsin; 1.

R Pfam; PF00008; trypsin; 1.

R Pfam; PF00084; sushi; 2.

R Pfam; PF00089; trypsin; 1.

R PRINTS; PR00722; CHYMOTRYPSIN.

R SMART; SM00032; CCP; 2.

R SMART; SM00032; Tryp_SPc; 1.

R SMART; SM00020; Tryp_SPc; 1.

R SMART; SM00020; Tryp_SPc; 1.

R R SMART; SM00010; ASX_HYDROXYL; UNKNOWN_1.

R PROSITE; PS01180; CUB; 2.

R PROSITE; PS01180; CGF_2; 1.

R PROSITE; PS01187; EGF_CA; 1.
    Matches
               Query Match
Best Local Similarity
                                                                                        InterFo; IPR000152; Asx_hydroxyl.
InterFor; IPR000859; CUB_domain.
InterPro; IPR000861; EGF-like.
InterPro; IPR000861; EGF_Ca.
Pfam; PF00431; CUB; 2.
SMART; SM00042; CUB; 1.
SMART; SM0010; ASX_HYDROXYL; UNKh PROSITE; PS001180; CUB; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
Calcium-binding; EGF-like domain; Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      009020;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ra-reactive factor serine protease pl00 (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                        ab. Invest. 0:0-0(1997).

- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL: AF004661; AAB65832.1; -.
HSSP: P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                     Knittel T., Fellmer P., Neubauer
Ramadori G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   009020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fy match
t Local Similarity 51.6
ches 16; Conservative
                                                                                                                                                                                                                                                            MEROPS; S01.198;
                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                         "The complement
                                                                                                                                                                                                                                                                                                                                           nd is induced
                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              ivo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 LFGRISSPGFPKPYSNDLTMNWNIKVPEGYR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serine protease.
E 688 AA; 77513 MW;
                                                      212
212 AA;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                           t activating protease by IL-6 in vitro and
                                                      212
24377 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.0%;
51.6%;
               39.1%;
45.2%;
 : Score 93; DB
: Pred. No. 0.00
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 100; DB 13;
Pred. No. 0.00014;
5; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180DD559EF8B6573
                                                     1882F52BF0D30A7E
                                                                                                                                                 UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                 ×.
                                                                                           Glycoprotein;
                                                                                                                                                                                                                                                                                                                                        p100 is
                                                                                                                                                                                                                                                                                                                                                                                 Kawakami M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212
                            DB 11;
               .00029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₹
                                                                                                                                                                                                                                                                                                                                                      expressed
                         Length 212;
                                                                                                                                                                                                                                                                                                                                           acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
                                                      CRC64;
                                                                                           Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 688;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                 Grundmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                         phase
                                                                                                                                                                                                                                                                                                                                                      hepatocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protease;
                                                                                                                                                                                                                                                                                                                                                                                 Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
0,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus
Gaps
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RESULT 16
Q9JJS9
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                                                                                             БР
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                                            Query Match
Best Local S
Matches 14
                                                                                                                                                        Pfam; pF00084; sushi; 2.

Pfam; pF00084; sushi; 2.

Pfam; pF00089; trypsin; 1.

PRIMIS; pR00722; CHYMOTRYPSIN.

SMART; SM00032; CCCP; 2.

SMARR; SM000032; CCCP; 2.

SMARR; SM000020; Tryp_SPC; 1.

SMART; SM00101; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; pS01180; CUB; 2.

PROSITE; pS01180; CUB; 2.

PROSITE; PS01180; EGF_2; 1.

R PROSITE; PS01187; EGF_CA; 1.

R CALCLUM-binding; EGF-11ke domain; Glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9JJS9 PRELIMINARY;
Q9JJS9;
Q9JJS9;
Q1-OCT-2000 (TrEMBLrel. 1:
01-OCT-2000 (TrEMBLrel. 1:
01-JUN-2002 (TrEMBLrel. 2:
Mannose-binding protein a:
                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR0001314; Chymotrypsin.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ277423; CAB89695.1; HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MASP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; S01.198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20469449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                    Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment).
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            21
 29
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MFGQIQSPGYPDSYPSDSEVTWNITVPEGFR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEGQIQSPGYPDSYPSDSEVTWNITVPEGFR
                                             l Similarity 45.2
                                                                                                                                                    Serine protease; Signal.
                                                                                          701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 21,
                                                                                                                   <1
22
                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10913141;
                                                                                                                  21
701
                                                    39.1%;
                                                                                            79663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15, Created)15, Last sequence update)21, Last annotation update)associated serine protease-1
                                                                                            Ψ.
                                           ; Score 93; DB; Pred. No. 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                .'
                                                                                                     MANNOSE-BINDING PROTEIN ASSOCIATED PROTEASE-1.
                                                                                                                              POTENTIAL
                                                                                          B5CFD619D63CE3DD CRC64;
                                                                                                                                                               Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
                                                        DB 11;
0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                              10;
                                                                                                                                                               Hydrolase;
                                                                   Length 701
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor
                                                                                                                                                                Protease;
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QQ AC 
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96RS4;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                        STRAIN=BALB/C; TISSUE=LIVER; Takahashi M., Miura S., Ishii N., Endo Y., Matsushita M., Fujita T.;
                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MBL-associated serine protease-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS01187; EGF_CA; UNKNOWN_1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
                                                                              Submitted (OCT-2000) to the EMBL; AB049755; BAB69688.1;
                                                                                                                               "An essecial role of MBL-associated serine activation of complement by lectin pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00431; CUB; 2.
Pfam; PF00084; sushi; 2.
Pfam; PF00089; trypsin; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF284421; AAK84071.1; -...
nterPro; IPR000152; Asx_hydroxyl.
nterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF Ca.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR00036; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding lectin complement activation Immunity 15:127-135(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dahl M.R., Thiel S., Matsushita M., Fujita T., Willis & Christensen T., Vorup-Jensen T., Jensenius J.C.;
"Masp-3 and its association with distinct complexes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=21378425; PubMed=11485744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 1 01-JUN-2002 (TrEMBLrel. 2 Complement factor MASP-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q96RS4
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                        MASP1 OR MASP3
                              MEROPS; S01.132; -.
MGD; MGI:88492; Masp1.
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 VFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MFGQIQSPGYPDSYPSDSEVTWNITVPDGFR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
     IPR000152; Asx_hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine protease. 728 AA; 81860 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.1%;
45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81860 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19,
19,
21,
                                                                                                        EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 93; DB Pred. No. 0.00 7; Mismatches
                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09B5297A6C14283A CRC64;
                                                                                                                                                                                                      Sugamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T., Willis A.C J.C.;
                                                                                                                                         protease-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 728;
                                                                                                                                                                                                    Shuichi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the mannan-
                                                                                                                                                        3
                                                                                                                                                                                                      Shiro
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                                                                                                                                                                                                                                                                                                                              Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                            RESULT 20
Q9UC48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 19
Q8TD25
       밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                  Q9UC48 PRELIMINAKY;
Q9UC48;
01-MAY-2000 (TrEMBLrel. 13, C)
01-MAY-2000 (TrEMBLrel. 14, L)
01-JUN-2000 (TrEMBLrel. 14, L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8TD25;
Q8TD25;
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY038048; AAK71497.1; -. SEQUENCE 996 AA; 107585 MW; E8012D30969D925E CRC64;
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                              VI-MAI-2000 (TEEMBLEEL 13, Last sequence update) 01-JUN-2000 (TEEMBLEEL 14, Last annotation updat 18.5 kDa tumor marker protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE: PS01180; CUB; 2.
PROSITE: PS01187; EGF_2; UNKNOWN_1.
PROSITE: PS01187; EGF_CA; UNKNOWN_1.
PROSITE: PS0240; TRYPSIN_DOM; 1.
PROSITE: PS00135; TRYPSIN_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00431; CUB; 2.
Pfam; PF00084; sushi; 2.
Pfam; PF00089; trypsin; 1.
SMART; SM00181; EGF; 1.
MEDIINE=96212543; PubMed=8618346;
Rasmussen H.H., Orntoft T.F., Wolf H.,
"Towards a comprehensive database of pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase;
SEQUENCE
                                                                         SEQUENCE
                                                                                                                                                                                                      Homo sapiens (Human).
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IPR000561; EGF-like.
IPR001881; EGF-Ca.
IPR001284; Ser_protease_Try.
IPR000436; Sushi_SCR_CCP.
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nilarity 40.4%;
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82373 MW; 6B917743118941C1 CRC64;
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Pred. No. 0.0028;
3; Mismatches 13;
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7; Mismatches
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Catarrhini; Hominidae;
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                            Celis J.E.;
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			Search completed: January 11, 2003, 10:51:43 Job time : 125 secs	Oy 15 LASPGEPGEYANDQER 30	Query Match 36.6%; Score 87; DB 4; Length 16; Best Local Similarity 100.0%; Pred. No. 8.5e-05; Matches 16; Conservative 0; Mismatches 0; Indels 0	RT patients with bladder cancer."; RL J. Urol. 155:2113-2119(1996). SQ SEQUENCE 16 AA; 1751 MW; 289540537A1B4400 CRC64;
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Result
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Copyright (c) 1993 - 2003 Compugen
 TLD_BRARE
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NRP1_HOUSE
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NRP1_HUMAN
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Q04670 saccharomyc P47100 saccharomyc		pyr		055123 mus musculu	042632 cochliobolu	×		thermopla	Q8zfr0 yersinia pe		P05997 homo sapien		Q09233 caenorhabdi	P47845 oryctolagus			P98068 strongyloce	paracentro			P98065 oryctolagus	Q07806 pseudomonas	Q9r172 rattus norv	homo	P98066 homo sapien

## ALIGNMENTS

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SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE=99192764; PubMed=10092804;  Stover C.M., Thiel S., Thelen M., Lynch N.J., Vorup-Jensen T.,  Jensenius J.C., Schwaeble W.J.;  Jensenius J.C., Schwaeble W.J.;  "Two constituents of the initiation complex of the mannan-binding lectin activation pathway of complement are encoded by a single	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  Thiel S., Vorup-Jensen T., Stover C.M., Schwaeble W., Laursen S.B., Poulsen K., Willis A.C., Eggleton P., Hansen S., Holmskov U., Reid K.B.M., Jensenius J.C.;  Reid K.B.M., Jensenius J.C.;  "Identification and characterization of a novel protein of the human complement system, mannan-binding lectin-associated serine protease-2 (MASP-2).";  Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  SEQUENCE:  TISSUE-Liver;  MEDLINE-97242412; PubMed-9087411;  Thiel S., Jensen T.V., Stover C.M., Schwaeble W.J., Laursen S.B.,  Poulsen K., Willis A.C., Eggleton P., Hansen S., Holmskov U.,  Reid K.B.M., Jensenius J.C.;  "A second serine protease associated with mannan-binding lectin that activates complement.";  Nature 386:506-510(1997).	(Rel. 39, (Rel. 41, ing lectin nding prot ated serin s (Human). s (Human). s (Human).	T 1 HUMAN MAS2_HUMAN CO01187; C75

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PROSITE; PS0010; ASX_ni...

PROSITE; PS01180; CUB; 2.

RROSITE; PS01186; EGF_2; 1.

R PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS001187; EGF_CA; 1.

R PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.

DR PROSITE; PS00134; TRYPSIN_SER; 1.

CROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00136; TRYPSIN_SER; 1.

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InterPro;
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SMART; SM00032; CCP; 2.
MART; SM00042; CUB; 2.
MART; SM000179; EGF_CA; 1.
MART; SM00020; Tryp_SPC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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EMBL; X98400; CAA67050.1;
EMBL; Y18287; CAB50735.1;
EMBL; Y18286; CAB50733.1;
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                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Park D.,
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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AF321558; AAG50274.1; JOINED.
AF321559; AAG50274.1; JOINED.
AF321560; AAG50274.1; JOINED.
AF321561; AAG50274.1; JOINED.
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                                                                                                                                                                                                                                                                                                     ; Sushi;
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CUB_domain.
Chymotrypsin.
EGF-like.
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Sushi_SCR_CCP.
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SUSHI 2.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                             CUB
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                                                                                                                                                     EGF-LIKE,
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                                                                                                                                                                                                                                               MANNAN-BINDING
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              TISSUE=Placenta;
MEDLINE=97079701; PubMed=8921412;
Endo Y., Sato T., Matsushita M.,
                                                                                                                                                                                                                                                                                                            CRAR_HUMAN STANDARD; PRT; 699 AA.
P48740; 095570; Q9UF09;
01-FEB-1996 (Rel. 33, Created)
15-GCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Complement-activating component of Ra-reactive factor precursor
(EC 3.4.21.-) (Ra-reactive factor serine protease p100) (RaRF)
(Mannan-binding lectin serine protease 1) (Mannose-binding prote
associated serine protease) (MASP-1).
MASP1 OR CRARF OR CRARF1 OR PRSS5.
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Engo Y., Sato T., Matsushita M., Fujita T.; "Exon structure of the gene encoding the human mannose-binding protein-associated serine protease light chain: comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                               _HUMAN
                                                                                 Sato T., Endo Y., Matsushita M., Fujita T.; "Molecular characterization of a novel serine protease involved activation of the complement system by mannose-binding protein." Int. Immunol. 6:665-669(1994).
                                                                                                                                                                         Takada F., Takayama Y., Hatsuse H., Kawakami M.;
"A new member of the C1s family of complement proteins found bactericidal factor, Ra-reactive factor, in human serum.";
Biochem. Biophys. Res. Commun. 196:1003-1009(1993).
                                                                                                                            MEDLINE=94289349; PubMed=8018603;
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 TISSUE=Liver;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
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                                                            SEQUENCE FROM
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D -> Y (IN REF. 4).
L -> LCS (IN REF. 4).
G -> E (IN REF. 4).
G -> E (IN REF. 4).
MISSING (IN REF. 3).
L -> LIL (IN REF. 3).
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Pred No. 1.8e-20;
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RELAY SYSTEM (BY SIMILARITY).
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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Int. Immunol. 8:1355-1358(1996)
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SUBUNIT: RARF CONSISTS OF A COMPLEMENT-ACTIVATING COMPONENT (CRARF) AND A POLYSACCHARIDE-BINDING (MANNOSE-BINDING) COMPONENT CRARF IS AN HETERODINER OF A HEAVY (P70) AND A LIGHT CHAIN (P29) LINKED BY A DISULFIDE BOND.

DOMAIN: CRARF HAS A MODULE ORGANIZATION SIMILAR TO C1R AND C1S.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                         L; AB007617; BAAB9206.1; JOINED.
L; AB007602; BAAB9206.1; JOINED.
L; AB007603; BAAB9206.1; JOINED.
L; AB007604; BAAB9206.1; JOINED.
L; AB007605; BAAB9206.1; JOINED.
L; AB007606; BAAB9206.1; JOINED.
L; AB007607; BAAB9206.1; JOINED.
L; AB007608; BAAB9206.1; JOINED.
L; AB007609; BAAB9206.1; JOINED.
L; AB007610; BAAB9206.1; JOINED.
L; AB007611; BAAB9206.1; JOINED.
L; AB007612; BAAB9206.1; JOINED.
L; AB007613; BAAB9206.1; JOINED.
L; AB007614; BAAB9206.1; JOINED.
L; AB007615; BAAB9206.1; JOINED.
L; AB007616; BAAB9206.1; JOINED.
L; AB007615; BAAB9206.1; JOINED.
L; AB007615; BAAB9206.1; JOINED.
L; AB007616; BAAB9206.1; JOINED.
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L; AB010814; BAA34864 1; JOINED.
L; AB010815; BAA34864 1; JOINED.
L; AB010816; BAA34864 1; JOINED.
L; AB010817; BAA34864 1; JOINED.
L; AB010818; BAA34864 1; JOINED.
L; AB010819; BAA34864 1; JOINED.
L; AB010820; BAA34864 1; JOINED.
L; AB010821; BAA34864 1; JOINED.
L; AB010821; BAA34864 1; JOINED.
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HGNC:6901; MASP1.
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IPR000152; Asx_hydroxyl.
IPR000859; CUB_domain.
IPR001314; Chymotrypsin.
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THE C4 AND C2 COMPONENTS. IT ACTIVATES THE
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MFGQIQSPGYPDSYPSDSEVTWNITVPDGFR

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SMART; SM00101; EGF; 1.

SMART; SM00179; EGF_CA; 1.

SMART; SM00179; EGF_CA; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS001180; CUB; 2.

PROSITE; PS01180; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS0134; TRYPSIN_DOM; 1.

PROSITE; PS0134; TRYPSIN_HIS; 1.
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Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00089; trypsin; 1.
Pfam; PF00431; CUB; 2.
PRINTS; PR00722; CHYMOTRYPSIN..
                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                      CARBOHYD
                                                                                                                                                CARBOHYD
                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                         ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [nterPro;
           Local
                     Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00084; sushi;
   14;
  Similarity 45.
|4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000561;
IPR001881;
IPR001254;
IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sushi,
                                       ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                        699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF-like.
EGF_Ca.
Ser_protease_Try.
Sushi_SCR_CCP.
                                      79258
            45
          39.1%;
45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat;
                                       Œ;
                                            N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
Q >> E (IN REF. 1)...
A -> G (IN REF. 3)...
K -> G (IN REF. 3)...
K -> A (IN REF. 3)...
D -> A (IN REF. 1)...
D -> V (IN REF. 3)...
Q -> K (IN REF. 3)...
Q -> K (IN REF. 3)...
D -> V (IN REF. 3)...
                                                                                                                                                                                                                         POTENTIAL POTENTIAL POTENTIAL
                                                                                                                                                                                                                                                                                                                                             SUSHI 1.
SUSHI 2.
                                                                                                                                                                                                                                                                                                                                                     CUB 2
SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; E
                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                          CHARGE RELAY SYSTEM (BY SI)
CHARGE RELAY SYSTEM (BY SI)
CHARGE RELAY SYSTEM (BY SI)
HYDROXYLATION (POTENTIAL)
           Pred.
                   Score 93;
                                                                                                                                                                                                                                                                                                                                                                                 CUB 1
                                                                                                                                                                                                                                                                                                                                                                                         RA-REACTIVE FACTOR.
70 KDA CHAIN OF P100
29 KDA CHAIN OF P100
                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                   SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                       EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENT-ACTIVATING COMPONENT
                                                                                                                                                        N-LINKED
                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                    INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                         Serine protease; Proteasin; ignal; EGF-like domain;
                                        ADD9697AE6AB01B5
  Mismatches
          Ö
                                                                                                                 (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
IN REF. 1 AND
                                                                                                                                                     (GLCNAC. .
           DB 1;
0.0016;
                                                                                                                                                                                    (POTENTIAL).
10;
                 Length 699
                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protease;
                                                                                                                                                                                                                                                                                                     (BY SIMILARITY)
(BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                          (P70).
(P29).
  Indels
                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydroxylation
  0
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  Gaps
 0
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CRAR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                       MGD; MGI:8849; Masp1.
InterPro; IPR000152; Asx_hydroxy1.
InterPro; IPR000859; CUB_domain.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001254; Ser_protease_Tr
InterPro; IPR001254; Sushi_SCR_CCP.
Pfam; PF00084; Sushi; 2.
                                                                                                                                                                                                                                                                                            his SWISS-PROT entry is copyright. It is produced through a collaboration etween the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformaticy Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOCHEM. BIOPHYS. Res. COMMUN. 190:681-687(1993).

-I- FUNCTION: COMPONENT OF THE BACTERICIDAL FAR-REACTIVE FACTOR RARF WHICH SPECIFICALLY BINDS TO RA AND R2 POLYSACCHARIDES EXPRESSED E CERTAIN ENTEROBACTERIA. IT TRIGGERS THE ACTIVATION OF COMPLEMENT CASCADE BY ACTIVATING THE C4 AND C2 COMPONENTS. IT ACTIVATES THE C4 C4 COMPONENT BY CLEAVING THE ALPHA-CHAIN OF C4.

-i- SUBUNIT: RARF CONSISTS OF A COMPLEMENT-ACTIVATING COMPONENT (CRARF) AND A POLYSACCHARIDE-BINDING (MANNOSE-BINDING) COMPONENT. CEARF IS AN HETERODIMER OF A HEAVY (P70) AND A LIGH CHAIN (29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P98064;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Complement-activating component of Ra-reactive factor precursor (EC 3.4.21.-) (Ra-reactive factor serine protease p100) (RaRF)
(Mannan, Ding)
                             Pfam;
Pfam;
                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A 100 kDa protein in the C4-activating actor is a new serine protease having more careful.
                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93176166; PubMed=8439319;
Takahashi A., Takayama Y., Hatsuse H.,
"Presence of a serine protease in the «
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   orkalN=BALB/c; TISSUE=Liver;
MEDLINE=94179811; PubMed=813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 465-704 FROM N.A.,
             PRINTS;
                                                                                                                                                                                                        MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MASP1 OR CRARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRAR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resence of a serine protease in the complement-activating component the complement-dependent bactericidal factor, RaRF, in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunol. 152:2308-2316(1994).
                           PF00089; trypsin; 1. PF00431; CUB; 2.
                                                                                                                                                                                                                     P00736;
                                                                                                                                                                                                                                       D16492; BAA03944.1;
SM00032;
                                                                                                                                                                                                      S01.198;
              PR00722;
                                                                                                                                                                                                                     1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
CCP;
             CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND PARTIAL SEQUENCE.
                                                           Ser_protease_Try.
Sushi_SCR_CCP.
; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takahashi A., Kawakami M.;
                                                                                                                                                                                                                                       .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          having module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawakami M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         component of Ra-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           C1R AND C1S
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RESULT
TOH2_C/
  RRA COCC
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SMART; SM00179; EGF_CA; 1.

SMART; SM00020; Tryp_SPC; 1.

R PROSITE; PS0010; ASX_HYDROXYL; 1.

R PROSITE; PS01186; EGF_2; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01187; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

"""Arnlase; Complement pathway; Se
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                Query Match
                                                                       DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                              DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
ACT_SITE
ACT_SITE
ACT_SITE
MOD_RES
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                       DISULFID DISULFID
                                                                Zinc metalloproteinase
TOH-2 OR R151.5.
Caenorhabditis elegans.
                                                                                                                                 CAEEL
                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
       Fulton L.
Submitted (FEB-1994) to the
                STRAIN=Bristol N2;
                        SEQUENCE FROM N.A.
                                               Rhabditidae;
                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                         4
                                                                                                                                                                32 MFGQIQSPGYPDSYPSDSEVTWNITVPEGFR
                                                                                                                                                                               11 VFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                         Local
                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                 704
                                                                                                                                                                                                Conservative
                                                Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sushi;
                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                       Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                                                                                                                                                                                        39.1%;
45.2%;
                                                                                                                                                                                                                               79895 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat;
                                                                                                                                                                                                                              N-LINKED (GLCNAC. ..) (
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RA-REACTIVE 1
70 KDA CHAIN
29 KDA CHAIN
                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
INTERCHAIN
                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                               CUB 1.
EGF-LIKE,
                                                                                                                                                                                                                                                                                                                                                                                      CHARGE
CHARGE
                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                Score 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       signal;
                                                                                                                                                                                                                                                                                                                                                                      HYDROXYLATION POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                      CHARGE RELAY
                                                                                                                                                                                                                                                                                                                                                                                                              SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENT-ACTIVATING COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDA CHAIN
                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                         No.
                                                                                                                                                                                                                                                                                                                                                                                      E RELAY SYSTEM
E RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                              PROTEASE
                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e protease;
EGF-like do
                                                                                 update)
r (EC 3.4.24.-).
                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                               CALCIUM-BINDING
                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                        0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ဝှ ဝှ
                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                P100
                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain;
                                                                                                                                                                                                               Length 704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease
                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (P70).
(P29).
                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydroxylation
                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QF
                                                                                                                                                                                                Gaps
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RESULT 5
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   SSCEPPPAL
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                                                                                                                                                                                                                                           SQ
                                                                                                                                                                                            Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; RI51.5; CE27200.
InterPro; IPR001506; Astacin.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000861; EGF-like.
InterPro; IPR000884; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF00090; tsp_1; 1.
Pfam; PF000431; CUB; 1.
Pfam; PF004431; CUB; 1.
Pfam; PF001400; ASTACIN.
SMART; SM00001; EGF-like; 1.
SMART; SM00001; EGF-like; 1.
SMART; SM00001; EGF-like; 1.
SMART; SM00235; ZnMC; 1.
                                           C1R_HUMAN
P00736;
21-JUL-1986
01-AUG-1988
15-JUN-2002
                                                                                                                                                                                                                                         CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                               ETAL
ETAL
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PROSITE;
                          Complement Clr Clr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.;
Submilted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
-!- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
-!- SIMILARITY: BELCNGS TO PEPTIDASE FAMILY M12A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
REVISIONS.
                                                                                                                                                                                                                                                                                                             METAL
                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50092; TSP1; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U00036; AAK29859.1; -. SSP; P28825; 1IAF. EROPS; M12.UPA; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
             Homo sapiens (Human)
                                                                                                                                                   383
                                                                                                                                                                                                                                                                                                 CT_SITE
                                                                                                                                                                      14 RLASPGFPGEYANDQERRWTLTAPPGY 40
                                                                                                                                                  RISSPGYPREFKEGQECSWLLVAPPGH 409
                                                                                                                                                                                             l Similarity
14; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                PS00022;
PS01186;
                                                                                                                                                                                                                                                                                                                                                                                                                                      PS01180;
                                                                                                                                                                                                                                        19
321
371
371
490
222
223
223
226
232
167
438
592 4
  Metazoa;
                                             (Rel. 01, Created)
(Rel. 08, Last seq
(Rel. 41, Last ann
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                         AA;
                                 component
                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              EGF_1; 1.
EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     CUB;
                                                                                                                                                                                                                                                                18
592
361
487
541
522
223
223
167
  Chordata;
                                                                                                                                                                                                         35.7%;
51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zn_MTpeptdse.
                                Last sequence update)
Last annotation update)
ent precursor (EC 3.4.21.41).
                                                                                                                                                                                                        . 98;
                                                                                                                                                                                                                                           ME:
                                                                                                                                                                                                                                                          TSP TYPE-1.
ZINC (CATALYTIC) (
BY SIMILARITY.
ZINC (CATALYTIC) (
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Craniata;
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MEDLINE-8702666; PubMed-3021205;
between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i
                                                                   This
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-i- FUNCTION: C1R B CHAIN IS A SERINE PROTEASE AND C1S TO FORM C1. THE FIRST COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                          Bersch B., Hernandez J.-F., Marion D., "Solution structure of the epidermal gof human complement protease Clr, an a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arlaud G.J.; "Identification of a cryptic protein kinase CK2 phosphorylation site in human complement protease Clr, and its use to probe intramolecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 133-137; 187-211 AND 609-613, AND MEDLINE-96221263; PubMed-8635594; Pelloux S., Thielens N.M., Hudry-Clergeon G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87241248: pubMed=3036070; Arlaud G.J., Willis A.C., Gagnon J.; "Complete amino acid sequence of the classical-pathway enzyme Cir."; Biochem. J. 241:711-720(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; NCBI_TaxID=9606; [1]
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MEDLINE-98138432; PubMed-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement subcomponent C1-r.";
Biochemistry 22:1758-1764(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification of erythro-beta-hydroxyasparagine domain of human Clr.";
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Biochem. J. 240:783-787(1986).
                                                                                                                                                                                                                                                                                                                                                                                              family."
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                                                            SWISS-PROT entry is copyright. It is produced through
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l growth factor (E
n atypical member
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MART; SM00032; CCP; 2.
JMART; SM00042; CUB; 2.
SMART; SM000179; EGF_CA; 1.
SMART; SM00020; Tryp_SPc;
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2; PS00022; EGE_1; FALSE_N
2; PS01186; EGE_2; 1.
3; PS01187; EGE_CA; 1.
3; PS0134; TRYPSIN_HIS; F
2; PS00134; TRYPSIN_SER; 1
Similarity
15; Conser
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IPR001314; Chymotrypsin.
IPR001561; EGF-like.
IPR001881; EGF_Ca.
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IPR000436; Sushi_SCR_CCP.
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0; ASX_HYDROXYL;
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phorylation; Sushi; Repeat; Signal;
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44.1%;
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CHARGE RELAY SYSTEM.
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5CBCCC0201061463 CRC64;
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GLCNAC ..).
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                                                 "Post-translational proteolytic processing of procollagen C-
proteinase enhancer releases a metalloproteinase inhibitor."
J. Biol. Chem. 275:1384-1390(2000).
-:- FUNCTION: BINDS TO THE COOH-TERMINAL PROPEPTIDE OF TYPE
                                                                                                                                                                        Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S., "Structural organization and expression patterns of the human and mouse genes for the type I procollagen COOH-terminal proteinase enhancer protein.";
Genomics 55:229-234(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCO1_HUMAN STANDARD; PRT; 449 AA.
Q15113; O14550;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2000 (Rel. 41, Last annotation update)
Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I procollagen C-proteinase enhancer) (Type 1 procollagen C-proteinase enhancer)
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Morisaki N., Saito Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identification, primary structure, and
cognate human gene (PCOLCE).";
J. Biol. Chem. 269:26280-26285(1994).
                                                                                                                                  PARTIAL SEQUENCE, MEDLINE-20092917;
                                                                                                                                                                                                                                        TISSUE=Placenta;
MEDLINE=99134301; PubMed=9933570;
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"Type I procollagen COOH-terminal
identification, primary structure,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                          Banda M.J.
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Jani-Sait S., Shows T.B., Greenspan D.S.;
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           PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-FUNCTION: C-TERMINAL PROCESSED PART OF METALLOPROTEINASE INHIBITORY ACTIVITY.
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Struct. Funct. 21:662-662(1996).
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. 8:1060-1073(1998).
                                                                                                                     Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     observations
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                                                                                                                   AND CHARACTERIZATION OF INHIBITORY ACTIVITY PubMed=10625689; C.L., Rosenbach M.T., Takahara K., Greenspa
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                                      C-PROTEINASE
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DOMAIN
                                                                      SEQUENCE FROM N.A.
MEDLINE-8901/187; PubMed-2459702;
MEDLINE-8901/187; PubMed-2459702;
Kusumoto H., Hirosawa S., Salier J.P.,
"Human genes for complement components
tail-to-tail arrangement.";
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nterPro: IPR001134: Netrin_C.
/fam; PP00431; CUB; 2.
Pfam; PF01759; NTR; 1.
SMART; SM00042; CUB; 2.
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11S.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A. TISSUE*Liver;
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-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                         Hagen F.
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Spycher S.E., Nick H., Rickli E.E.;
"Human complement component Cls. Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tosi M., Duponchel C., Meo T., Couture-To "Complement genes Clr and Cls feature an domain closely related to haptoglobin."; J. Mol. Biol. 208:709-714(1989).
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linkage of the homologous genes Cls and Clr.";
Biochemistry 26:8516-8524(1987).
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Biochemistry 30:2827-2833(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Illy C., Thielens N.M., Gagnon J., Arlaud G.J.; "Effect of lactoperoxidase-catalyzed iodination on the \text{Ca}(2+)-dependent interactions of human Cls. Location of the iodination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The serine proteinase chain of human complement component Cyanogen bromide cleavage and N-terminal sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the heavy chain and activation.";
Dragon-Durey M.-A.,
de Barace C., Prieu
                                           PubMed=11390518;
                                                                                                                                            Rossi V., Gaboriaud C., Lacroix M.,
Gagnon J., Arlaud G.J.;
"Structure of the catalytic region
study by chemical cross-linking and
                                                                                                                                                                                                                                    PARTIAL SEQUENCE, MEDLINE=95298736;
                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry
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"Two lineages of mannose-binding
                                                                                                         Biochemistry
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    Prieur
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C A.-M., Weiss
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Fremeaux-Bacchi
s L., Fridman W.-
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Pfam; PF000084; sushi; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF000431; CUB; 2.
Pfam; PF00431; CUB; 2.
Pfam; PF00432; CCF; 2.
Pfam; SM00032; CCF; 2.
SMART; SM00042; CUB; 2.
SMART; SM00109; EGF_CA; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X06596; CAA29817.1; -.
EMBL; J04080; AAA51853.1; -.
EMBL; M18767; AAA51853.1; -.
EMBL; AB009076; BAA86864.1; -.
PIR; A40496; C1HUS.
PIR; S00224; S00224.
MEROPS; S01.193; -.
SMISS-2DPAGE; P09871; HUMAN.
                                                                                                                                                                                                                               PROSITE;
PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muse by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular basis of a selective C1s deficiency associated with early onset multiple autoimmune diseases.";
                                                                                                               Calcium-binding
SIGNAL 1
                                                                                                                                           Complement pathway; 
Hydroxylation; Sush
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000859; CUB_domain.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001561; EGF-1ike.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 120580; -
                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:1247; C1S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a detween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: CLEAVES COMPONENT C4 TO C4A AND C4B, AND COMPONENT C2 TO C2A AND C2B.
SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R AND S IN THE MOLAR RATION OF 1:2:2. ACTIVATED C1S IS AN DISULFIDE-LINKED HETERODIMER OF AN HEAVY CHAIN AND A LIGHT CHAIN.
DISEASE: Defects in C1S are the cause of selective C1s deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISEASE: Defects in C1S are the cause of selective C1s d that is associated with early onset multiple autoimmune SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunol. 166:7612-7616(2001).

FUNCTION: C1S B CHAIN IS A SERINE PROTEASE THAT COMBINES WITH C1Q AND C1S TO FORM C1, THE FIRST COMPONENT OF THE CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. C1R ACTIVATES C1S SO THAT IT CAN, IN TURN, ACTIVATE C2 AND C4.
                                                                                                                                                                  E; PS00010; ASX_HYDROXYL; 1.
E; PS01180; CUB; 2.
E; PS00122; EGF_1; FALSE_NEG.
E; PS01186; EGF_2; FALSE_NEG.
E; PS01187; EGF_CA; 1.
E; PS50240; TRYPSIN_DOM; 1.
E; PS50240; TRYPSIN_HIS; FALSE.
E; PS00134; TRYPSIN_EER; 1.
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 16
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688
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172
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355
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                                                                                                                                           Plasma; Glycoprotein; Serine protease; Hydrolase;
i; Repeat; Signal; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asx_hydroxyl.
                                         EGF-LIKE,
CUB 2.
             SUSHI
                                                                                   COMPLEMENT
SERINE PROTEASE
                                                                                                                                          Signal;
                                                                                                                                                                                     FALSE_NEG.
              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                       CALCIUM-BINDING (POTENTIAL).
                                                                                   C1S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as its content
                                                                                   HEAVY
LIGHT
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                                                                                   CHAIN
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PRESENTATION OF THE PRESEN
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CONFLICT
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SEQUENCE
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MEDLINE-95014462; PubMed-7523404;

Takahara K., Kessler E., Biniaminov L., Brusel M., Eddy R.L.,

Jani-Sait S., Shows T.B., Greenspan D.S.;

"Type I procollagen COOH-terminal proteinase enhancer protein:
identification, primary structure, and chromosomal localization
cognate human gene (PCOLCE).";

J. Biol. Chem. 269:26280-26285(1994).
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961398; 035113;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Procollagen C-proteinase enhancer protein precursor (PCPE) (Type
procollagen COMH-terminal proteinase enhancer) (Type 1 procollagen
"Icoain E., Zelenika D., Laine M.C., Rhyne "Isolation of a novel cDNA corresponding the choroid plaxus and leptomeninges."; J. Neurochem. 56:2133-2138(1991).
                                                                                                                                                                           Hirahara I., Syoufuda K., Harada K., Tomita M., Urakami K.,
Morisaki N., Saito Y.;
"Smooth muscle cell derived procollagen C-protease enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                                              STRAIN=C57BL/6; TISSUE=CNS; MEDLINE=91225708; PubMed=2027019;
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                                                                                                                                                                                                                                             STRAIN=BALB/c;
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                                                                                                                       SEQUENCE FROM
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                                                                                                                                                              Struct. Funct.
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                                                                                                                                                                                                                                         TISSUE=Heart;
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Pred. No. 0.
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G -> GG (IN REF. 5).
T -> A (IN REF. 7).
TK -> GR (IN REF. 7).
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CHARGE RELAY SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROXYLATION (PROBABLE)
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                                       Rhyner T., Pessac B.; iding to a transcript expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                              chromosomal localization
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. 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 688;
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                                                                                                                                                                               enhancer protein.";
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RESULT 9
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Best Local
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CONFLICT
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DOMAIN
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EMBL; X57337; CAA40612.1; ALT_FRAME.
EMBL; X57337; CAA40612.1; ALT_FRAME.
MGD; MGI:105099; Pcolce.
InterPro; IPR001859; CUB_domain.
InterPro; IPR001134; Netrin_C.
                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                              Pfam; PF00431; CUB; 2: Pfam; PF01759; NTR; 1: SMART; SM00042; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ressler E., Mould A.P., Hulmes D.J.S.;
"Procollagen type I C-proteinse enhancer is a naturally occurring connective tissue glycoprotein.";
Blochem. Biophys. Res. Commun. 173:81-86(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Type I procollagen C-proteinase from mouse fibroblasts. Purification and demonstration of a 55-kDa enhancer glycoprotein."; Eur. J. Blochem. 186:115-121(1989).
                                                                                                                                   SEQUENCE
                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    lycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kessler E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90092088; PubMed=2689170, Kessler E., Adar R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [4]
CHARACTERIZATION.
                                                                                                                                                                                                                          ROSITE; PS01180; CUB; 2.
lycoprotein; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           npublished observations (JAN-2000).

1- FUNCTION: BINDS TO THE COOH-TERMINAL PROCOLLAGEN AND ENHANCES PROCOLLAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: EXPRESSED IN INTERSTITIAL CONNECTIVE TISSUES
LIKE TENDONS, CALVARIA, SKIN AND AT A LOWER LEVEL IN HEART AND
                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: PROCESSED FROM A 55 kDa FORM TO SIMILARITY: CONTAINS 2 CUB DOMAINS. SIMILARITY: CONTAINS 1 NTR DOMAIN.
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468
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N-LINKED (GLCNAC. . .)
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           PRT;
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                                                                                                     0.17;
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Pfam; PF00
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                                             PROSITE;
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Kessler E., Mould A.P., Hulmes D.J.S.;

"Procollagen type I C-proteinase enhancer is a naturally connective tissue glycoprotein.";

Biochem. Biophys. Res. Commun. 173:81-86(1990).

-i- FUNCTION: BINDS TO THE COOH-TERMINAL PROPERTIDE OF TYPE PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEINASE ACTION: SECRETED.

-i- SUBCELLULAR LOCATION: Secreted.

-i- SUBCELLULAR LOCATION: SECRETED AT HIGHEST LEVELS IN COUTSISUES, ESPECIALLY TENDON. ALSO EXPRESSED IN CORNEA AT SIMILARITY: CONTAINS 2 CUB DOMAINS.
                                                                                                                                                                                                           EMBL; AB008534; BAAZ3217.1; -. EMBL; AF015503; AAD01592.1; -. EMBL; AF016506; AAD01598.1; -. InterPro; IPR000859; CUB_domain. InterPro; IPR001134; Netrin_C.
                                                                                                                                                                                                                                                                                    EMBL; U94710; AAB93478.1;
EMBL; AB008534; BAA23217.1
EMBL; AF016503; AAD01592.1
                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a clother the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatical transfer of the statement is not removed. Usage by and formatical transfer of the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Masuda M., Igarashi H., Kano M., Yoshikura H.;
"Proviral integration into the procollagen C-proteinase
protein gene and its effects in cultured rat fibroblasts
an excisable 'hit-and-run' retroviral vector.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97447750; PubMed=9303490;
Ogata I., Auster A.S., Matsui A., Greenwel P., Geerts A., E
Ogata I., Kessler E., Rojkind M.;
"Up'regulation of type I procollagen C-proteinase enhancer
messenger RNA in rats with CC14-induced liver fibrosis.";
Hepatology 26:611-617(1997).
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Procollagen C-proteinase enhancer protein precursor (
procollagen COOH-terminal proteinase enhancer) (Type
                                                                                                                                            Pfam; PF01759; NTR; SMART; SM00042; CUB
                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hirahara I., Syoufuda K.,
Morisaki N., Saito Y.;
"Smooth muscle cell derive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91076903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Fischer 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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                                                                                                                                                                                          PF00431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria;
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                                          1 180; CUB;
Repeat; S
1 24
25 468
36
                                                                                                                                                                                            CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Aorta;
                                                                                                                                            CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=2256940;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein).
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                                                                                          Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harada K., Tomita
PROTEIN.
                                             PROCOLLAGEN C-PROTEINASE ENHANCER
                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-protease
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; Murinae; Rattus.
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procollagen
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RESULT 10
UVS2_XENLA
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Best Local :
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SEQUENCE
                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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11-NOV-1997 (Rel. 35, Last sequence update)
5-JUN-2002 (Rel. 41, Last annotation update)
5-JUN-2002 (Rel. 41, Last annotation update)
Embryonic protein UVS.2 precursor (EC 3.4.24.-).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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DOMAIN
                                                                                                          InterPro; IPR001506; Astacin.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000130; Zn_MTpeptds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UVS2
                                        SMART; SM00042; CUB; 2.
SMART; SM00235; ZnMC; 1.
                                                                                                                                                                                              EMBL; D89632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sato S.M.,
"Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression in hatching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Katagiri C., Maeda
Yasumasu S.;
                                                                   PRINTS; PR00480; ASTACIN.
                                                                                                                                                       MEROPS; M12.014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 196-514 FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                            Lecular approach to dorsoanterior development in Xenopus 1. Biol. 137:135-141(1990).

COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

DEVELOPMENTAL STAGE: EXCLUSIVELY IN THE ANTERIOR NEURAL F

NEURULA STAGE EMBRYOS. BY THE TAILBUD STAGE, THE PROTEIN

LOCALIZED IN SPECIALIZED CEPHALIZE ECTODERM, IN A REGION P

CORRESPONDING TO THE HATCHING GLAND.
                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A. SIMILARITY: CONTAINS 2 CUB DOMAINS.
                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                               PF00431; CUB; 2.
PF01400; Astacin; 1.
                                                                                                                                                                    P07584;
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            PS00142; ZINC_PROTEASE; PS01180; CUB; 2.
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352
28
454
468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cloning of Xenopus hatching enzyme and
in hatching gland cells.";
v. Biol. 41:19-25(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sargent T.D.;
Metalloprotease; Zinc; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                               ; BAA14003.1; -.
                                                                                                                                                                    liae.
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35.6%;
                                                                                                            Zn_MTpeptdse
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N-LINKED (GLCNAC. . .) (POTENTIAL)
; B4AA1C151323969B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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                                                                                                                                                                                                                                                                                           a collaboration - MBL outstation
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Best Local S
Matches 11
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the European Bioinformatics Institute. There are no use by non-profit institutions as long as its cont modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Mini fin protein).
TOLLOID OR TLD OR MFN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dorsal ventral patterning tolloid protein precursor (EC 3.4.24..)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
CHAIN
                                                                    This SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                                                                    Development 126:3119-3130(1999).
                                                                                                                                                                                                                                                                                                          Connors S.A., Trout J., Ekker M., Mullins M.C. "The role of tolloid/mini fin in dorsoventral
                                                                                                                                                                                                                                                                                                                                       FUNCTION, AND TISSUE SPECIFICITY. MEDLINE=99307076; PubMed=10375503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                              zebrafish embryo."
                                                                                                                                                                                                                                                                                                                                                                                "Cleavage of the BMP-4 antagonist Science 278:1937-1940(1997).
                                                                                                                                                                                                                                                                                                                                                                                                          Blader P., Rastegar
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98057457; PubMed=9395394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 SPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                            tailbud and cranial neural crest. At the 20-somite stage, also expressed in the hematopoletic system.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                            FUNCTION: Required for patterning ventral tissues of the tail. May increase bone morphogenetic protein (BMP) activity at the end of gastrulation by proteolytic cleavage of chordin and release of BMP from inactive complexes.

TISSUE SPECIFICITY: During gastrulation, accumulates around the
                                                                                                                                                                closing blastopore with greater expression ventrally. animal pole, expressed in the ectoderm flanking the anneural plate. At the 10-somite stage, expressed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPNYPGNYTTNTNCTWTITAPAGFK 439
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                                                     the Swiss Institute of Bioinformatics
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ZINC (CATALYTIC) (BY SIMILARITY).

N-LINKED (GLCANAC...) (POTENTIAL).

N-LINKED (GLCANAC...) (POTENTIAL).
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Pred.
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hordin by zebrafish Tolloid.";
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0.19;
                           There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                           pattern
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                                                                    collaboration
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SIGNAL
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PROSITE: PS001180; CUB; 5.
PROSITE: PS00022; EGF_1; FALSE_NEG.
PROSITE: PS01186; EGF_2; 2.
PROSITE: PS01187; EGF_CA; 2.
PROSITE: PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00008; EGF; 2.
Pfam; PF00431; CUB; 5.
Pfam; PF01400; Astacin; 1.
                                                                                    SEQUENCE
                                                                                                                                                                                              CARBOHYD
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SMART; SM00181; EGF; 2.
SMART; SM00179; EGF_CA; 2.
MART; SM00235; ZnMC; 1.
                                                                                                                                                                          CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR001881; EGF_Ca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [nterPro;
    Local Similarity
hes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF027596; AAC60304.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                email to license@isb-sib.ch).
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470
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  Pred. No. 0.3
B; Mismatches
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DORSAL-VENTRAL
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domain; Repeat; Signal; Glycoprotein;
                        NO.
                      0.38;
                                       DB 1;
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  RESULT 12
CASP_MESAU
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             Pfam; PF00008; EGF; 1.
Pfam; PF00084; SUSh1; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF000431; CUB; 2.
PF1NTS; PF00722; CHYMOTRYPSIN.
SMART; SM00032; CCCP; 2.
SMART; SM00042; CUB; 2.
SMART; SM00010; EGF_CA; 1.
SMART; SM001010; ASX_HYDROXYL; 1
PROSSITE; PS00010; ASX_HYDROXYL; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CASP_MESAU STAI
P15156;
01-APR-1990 (Rel. :
01-APR-1990 (Rel. :
15-JUN-2002 (Rel. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calcium-dependent serine proteinase precursor (EC 3.4.21.-) (CASP).
                                                                                                                                                                                                                           InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001561; EGF-like.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR001881; EGF_CCF_CCF.
InterPro; IPR001436; Sushi_SCR_CCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capable of degrading extracellular matrix protein FEBS Lett. 250:411-415(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.193;
                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S05008; S05008.
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X16160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinoshita H., Sakiyama H., Tokunaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mesocricetus.
NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: CAPABLE OF DEGRADING EXTRACELLULAR MATRIX PROTEINS CASP DEGRADES TYPE I AND IV COLLAGEN AND FIBRONECTIN IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isono K., Sakiyama S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89325606; PubMed=2753140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              792 GTISSPNWPDKYPSRKECTWDITATPGHR 820
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SUBUNIT: HETERODIMER, CONSISTING OF HEAVY AND LIGHT CHAINS WITH DISCULFIDE BONDS. THE HEAVY CHAIN IS EXPECTED TO BE A REGULATORY SUBUNIT AND THE LIGHT CHAIN CONTAINS THE CATALYTIC SITE.

DOMAIN: THE GLU-RICH REGION IN THE N-TERMINAL REGION MAY BE GAMMA CARBOXYLATED AND FUNCTION AS A CALCIUM-BINDING SITE.

SIMILARITY: TO BLOOD COAGGLATION FACTORS SUCH AS IX, X AND AN ANTICOAGGLATION FACTOR, PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRLASPGFPGEYANDQERRWTLTAPPGYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Imajoh-Ohmi S.,
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proteinase Hamada

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Best Local
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                                                                                                                                                                                                   BMP1_HUMAN STANDARD; PRT; 986 AA.
P13497; 013292; 099421; 099422; 099423; 014874; 090L38; Q13872;
01-JAN-1990 (Rel. 13, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
5-JUN-2002 (Rel. 41, Last annotation update)
5-JUN-2002 (Rel. 41, Last annotation update)
One morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld).
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ACT_SITE
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PROSITE;
PROSITE;
PROSITE;
                    Kriz
                                                                            is identical protein-1.";
                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM BMP1-3).
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                  HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Serine protease; Calcium-binding; Extracellular matrix; Gamma-carboxyglutamic acid; Vitamin K; Hydroxylation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                         Prockop D.J.
                                                                                                                                      TISSUE=Skin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                             Wozney J.M.,
                                       MEDLINE=89072730; PubMed=3201241;
                                                                                                                 Li S.W.,
                                                                                                                           MEDLINE=96209868;
                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
        Nozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitte Criz R.W., Hewick R.M., Wang E.A.;
Novel regulators of bone formation: molecular clones and
                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMAIN
                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                          9
                                                                                               C-proteinase that
                                                                                                                                                                                                                                                                                                                       EPTMHGEILSPNYPQAYPNEMEKTWDIEVPEGF
                                                                                                                                                                                                                                                                                                                                         EP-VFGRLASPGFPGEYANDQERRWTLTAPPGY 40
                                                                                                                                                                                                                                                                                                                                                            l Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00022;
PS01186;
PS01187;
PS50240;
PS00134;
                                                                                                                 Sieron A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00135;
                                                                                                                                                                                                                                                                                                                                                                                                  695
                                                                                                                                                                                                                                                                                                                                                                                                                 164
180
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181
297
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352
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137
155
1482
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1491
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                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                      to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                 AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF_CA; 1.
TRYPSIN_DOM; 1.
TRYPSIN_HIS; FALSE_NEG.
TRYPSIN_SER; 1.
                                                                   Sci.
                                                                                                                         PubMed=8643539;
                                              (ISOFORM BMP1-1).
                                                                                                                                                                                                                                                                                                                                                                                                413
77493
                                                                                                                                                                                                                                                                                                                                                                                                                   124
136
296
296
415
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178
178
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1536
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162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444
                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                    30.5%;
                                                                                                                  Fertala
                                                                                   processes procollagens to fibrillar collagens otein previously identified as bone morphogenio
                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                 WW.
                                                                                                                                                                                                                                                                                                                                                           Score 72.5; [
Pred. No. 0.39
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
OF CONTROL (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
1. E924F7E6340700D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUSHI 1.
SUSHI 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUB 2.
SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CALCIUM-DEPENDENT CALCIUM-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF-LIKE, CALCIUM-BINDING (POTENTIAL). HYDROXYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN.
GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALCIUM-DEPENDENT
                                                                                                                 A., Hojima Y.,
                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae
                                                                  93:5127-5130(1996)
                                                                                                                                                                                                                                                                                                                                                                    72.5;
No. 0.
                            Mitsock L.M., Whitters
                                                                                                                                                                                                                                                                                                                                                                    DB
.39;
                                                                                                                                                                         Hominidae;
                                                                                                                 Arnold W.V.,
                                                                                                                                                                                                                                                                                                                                                                             1:
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SERINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY
(BY)
(BY)
                                                                                                                                                                                                                                                                                                                                                                             Length 695;
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                   Euteleostomi;

⟨ SIMILARITY).
⟨ SIMILARITY).
⟨ SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEINASE.
PROTEINASE HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEINASELIGHT
                                                                                     morphogenic
                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                            1.
PROSITE; PROSITE; PROSITE; PROSITE; PROSITE;
                                                                                                                                                                                   MIM;
                                                                                                                                                                                           Genew;
                                                                                                                           InterPro;
                                                                                                                                    InterPro;
                                                                                                                                             InterPro;
                                                                                                                                                               InterPro;
                                                                                                                                                                        InterPro;
                                                                                                                                                                                                     MEROPS;
                                                                                                                                                       InterPro;
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SOTTTTTTTT

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EMBL; U50330; AAA93462.1; -.
EMBL; W22488; AAA51833.1; -.
EMBL; Y08723; CAA69973.1; -.
EMBL; Y08724; CAA69974.1; -.
EMBL; Y08725; CAA69975.1; -.
EMBL; L35278; AAC41703.1; -.
EMBL; L35279; AAC41701.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                  PRINTS; PRO0480; ASTACIN.
SMART; SM00042; CUB; 5.
SMART; SM00179; EGF_CA; 2.
SMART; SM00235; ZnMC; 1.
                                                                                                                                                                                                                        Pfam; PF000008; EGF; 2. Pfam; PF00431; CUB; 5. Pfam; PF01400; Astacin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahara K., Lyons G.E., Greenspan D.S.; "Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encoded by alternatively spliced transcripts which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differentially expressed in some tissues.";
J. Biol. Chem. 269:32572-32578(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98160316; PubMed=9500680;
Janitz M., Heiser V., Boettcher U., L
"Three alternatively spliced variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 242:1528-1534(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A37278; A37278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95096114; PubMed=7798260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alternative splicing.
TISSUE SPECIFICITY: UBIQUITOUS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND II. INDUCES CARTILAGE AND BONE FORMATION. CATALYTIC ACTIVITY: Cleavage of the C-terminal Ala-(-Asp in type I and II procollagens and at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENDOPEPTIDASE ENHANCER PROTEIN.
ALTERNATIVE PRODUCTS: 7 isoforms;
here), BMP1-4, BMP1-5, BMP1-6 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: BINDS 1 ZINC ION (BY ENZYME REGULATION: ACTIVITY IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 269:32572-32578(1994).
FUNCTION: CLEAVES THE C-TERMINAL PROPERTIDES OF PROCOLLAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         morphogenetic protein-1.";
ol. Med. 76:141-146(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                             112264;
                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:1067;
                                                                                         PS00142;
PS01180;
                         PS00022;
PS01186;
                                                                    PS00010;
                                                                                                                                                                                                                                                                                                                               IPR001506; Astacin.
IPR000152; Asx_hydroxyl.
IPR000859; CUB_domain.
IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                           IPR001881;
IPR000130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1APQ.
CUB; 5.

ASX_HYDROXYL; 2.

EGF_1; FALSE_NEG.

EGF_2; 2.

EGF_CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                               BMP1.
                                                                                                             ZINC_PROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISOFORMS
                                                                                                                                                                                                                                                                                                                 EGF_
                                                                                                                                                                                                                                                                                           Zn_MTpeptdse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BMP1-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
INCREASED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Landt O.,
ts of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BMP1-1,
BMP1-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lauster
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at Arg-|-Asp i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 produced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration
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no
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                                                               Query Match
Best Local S
Matches 13
                                                                                                                              VARSPLIC
CONFLICT
CONFLICT
SEQUENCE
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VARSPLIC
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VARSPLIC
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ACT_SITE
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metalloprotease;
 600
                              13
GSITSPGWPKEYPPNKNCIWQLVAPTQYR
                              GRLASPGFPGEYANDQERRWTLTAPPGYR
                                                                              Similarity
                                                                                                                           824
748
934
986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                           623
703
                                                                                                                                                                                                                                                                                                                                                                                                              303
589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zymogen;
                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine; Repeat; Bone; Cartilage; Hydrolase;
e; EGF-like domain; Zinc; Calcium; Signal;
                                                                                                                                            986
748
934
                                                                                                                              111248
                                                                            29.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.

ENC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC)

BY SIMILARITY.

BY S
                                                                                                                                X
X
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CUB 4.
CUB 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUB 1.
CUB 2.
EGF-LIKE 1,
CUB 3.
                                                                            Score 69;
Pred. No.
                                                                                                                                          PQEGSYLDFWDTHRGDPKPRRRKSLKTFSLTPÄTFRGIWA
L (IN ISOFORM BMP1-7).
MISSING (IN ISOFORM BMP1-7).
D -> N (IN REF. 4).
R -> S (IN REF. 4).
                                                                                                                                                                                                                          VKLTFMEMDIESQPECAYDHLEVFDGRDAKAPVLGRFCG
-> VLEGAGDRHSHLSGLELLLCPHALVDTVPAPPSALHGD
THAHTHTHVHTHCPIAQETCRGPPLGASRLSPQGPGHLTLA
                                                                                                                                                                                                                                                                                                           MISSING (IN ISÓFORM BMP1-5).

DKDECKSKNIGGCØD -> GGELFGLLGHPPRRP
ISOFORM BMP1-6).

MISSING (IN ISOFORM BMP1-6).
                                                                                                                                                                                                                                                                                                                                                                                         (IN ISOFORM BMP1-4).

MISSING (IN ISOFORM BMP1-4).

AACGGFLTKLNGSITSPGWPFKEYPPNKNCIWOLV

DLQVGKPLLWDRHCFRLSTHGPEMLGTALRG (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEYNFLKMEPQEVESLGETYDFDSIMHYARNTFSRGIFLDT
IVPKYEVNGVKPPIGQR -> VLHSSLLLLSCGSRNGASFP
CSLESSTHQALCWTGLFLRPSPFPRLPLAAPRTLRAGV
                                                                                                                                                                                                                                                                          EAGCDHKVTSTSGTITSPNWPDKYPSKKECTWAISSTPGHR
                                                                                                                                                                                                                                                                                        DKDECSKDNGGCQQDCVNTFGSYECQCRSGFVLHDNKHDCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BONE MORPHOGENETIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                        ISOFORM BMP1-5)
                                                                                                                         -> N (ÎN REF. 4).
-> S (ÎN REF. 4).
F89201913AC3CBEA CRC64;
                                                               Mismatches
628
                              41
                                                                                            DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALCIUM-BINDING
                                                               12;
                                                                                            Length 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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                                                             Gaps
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RESULT 14 BMP1\_MOUSE

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PRINTS; PRO0480; ASTACIN.
SMART; SM00142; CUB; 5.
SMART; SM00179; EGF_CA; 2.
SMART; SM00235; ZNMC; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS001180; CUB; 5.
PROSITE; PS00100; ASX_HYDROXYL; 2.
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS001187; EGF_CA; 2.
PROSITE; PS01186; EGF_CA; 2.
                                                                                                                                                                                                                                                                         InterPro; IPR00
InterPro; IPR00
Pfam; PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P98063;
01-FEB-1996
01-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;

"Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
which is related to the Drosophila dorsoventral gene tolloid and
encodes a putative astacin metalloendopeptidase.";

Dev. Biol. 163:175-183(1994),

-i- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II
AND II. INDUCES CARTILAGE AND BONE FORMATION.

-I- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
Ala-1-Asp in type I and II procollagens and at Arg-1-Asp in type
                                                                                                                                                                                                                                         Pfam; PF00008; EGF; 2.
Pfam; PF00431; CUB; 5.
Pfam; PF01400; Astacin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is use by non-profit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euxaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BMP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
(Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld).
               Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L24755; HSSP; P00736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6; TISSUE=Embryo; MEDLINE=94229342; PubMed=8174772;
                                                 Metalloprotease;
                                                                 Growth
                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                           MGD;
                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; M12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                       D; MGI:88176; Bmp1.

terPro; IPR001506; Astacin.

terPro; IPR000152; Asx_hydroxyl.

terPro; IPR000859; CUB_domain.

terPro; IPR000561; EGF-1ike.

terPro; IPR001881; EGF_Ca.

terPro; IPR00130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENDOPEPTIDASE ENHANCER PROTEIN.

TISSUE SPECIFICITY: AT HIGH LEVELS IN EMBRYONIC MATERNAL DECIDUUM
AND ELOOR PLATE REGION OF THE NEURAL TUBE. LESS IN DEVELOPING
AND ELOOR SAND ENDOCHONDRAL BONE, SUBMUCOSA OF INTESTINE, DERMIS
OF SKIN AND THE MESENCHYME OF SPLEEN AND LUNG.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COPACTOR: BINDS 1 ZINC ION (BY COPACTOR: BEGULATION: ACTIVITY IS
                                        E; PS01187; EGF_CA; 2.
factor; Cytokine; Repeat; Bone; oprotease; EGF-like domain; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                        .005;
; Zymogen.
1 25
26 125
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               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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INCREASED BY THE PROCOLLAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    991
                                                            Cartilage;
                                               Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                              Hydrolase;
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IN DEVELOPING
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tent is in no
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MP1_XENLA
DMP1_XENLA
DMP1_XENLA
DP8070;
AC P98070;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 40, Last annotation update)
None morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Eukaryota; Metazoa; Anura; Mesobatrachia; Pipoidea; Pipidae;
Venopodinae; Xenopus.
 В
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Matches 13
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CARBOHYD
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DISULFID
DISULFID
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DISULFID
                                                                                                                                                                                     TISSUE-Embryo;

MEDLINE-94085787; PubMed=8262384;

Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;

"Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic protein-1 during early embryonic development.";

Gene 134:257-261(1993).
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METAL
ACT_SITE
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                  between
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                                                                FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER DIFFERENTIATION OF DEVELOPING ORGANS.
DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED TADPOLES; LITTLE OR NO EXPRESSION IN MORULA AND LATE GASTRULA SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 3 CUB DOMAINS.
 European
            SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRLASPGFPGEYANDQERRWTLTAPPGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSITSPGWPKEYPPNKNCIWQLVAPTQYR
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Bioinformatics Institute.
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CUB 5.

ZINC (CATALYTIC)
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METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
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LINKED (GLCNAC. .
68A1847783A0BB9E
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There are no
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Pfam; PF00401; CUB; 3.
Pfam; PF01400; ASTACIN.
PRINTS; PR00480; ASTACIN.
SMART; SM00042; CUB; 3.
SMART; SM000179; EGF_CA; 1.
SMART; SM000235; ZDMC; 1.
PROSITE; PS00142; ZINC_PROTE
PROSITE; PS001180; CUB; 3.
PROSITE; PS001180; CUB; 3.
PROSITE; PS00010; ASX_HYDRO;
PROSITE; PS0001186; EGF_Z; 1.
PROSITE; PS001187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
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ACT_SITE
METAL
        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bone morphogenetic protein 1 homolog precursor (EC 3.4.24.-)
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocent
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CARBOHYD
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P98069;
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Strongylocentrotus
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Metalloprotease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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                                                                                                                                          563
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                                                                                                                                                      GRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                          GSINSPGWPKEYPPNKNCIWQLVAPTQYR 591
                                                                                                                                                                                 l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M12.005; ...
M12.005; ...
J. IPR001506; Astacin.
J. IPR000152; Asx_hydroxyl.
J. IPR000859; CUB_domain.
J. IPR000861; EGF-like.
J. IPR001881; EGF_CLA.
J. IPR001881; EGF_CLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000130; Zn_MTpeptdse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  equires a license agreement (See http://www.lsb-sib.ch/announce/email to license@isb-sib.ch).
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707
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398
398
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176
177
1180
180
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514
514
512
532
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1053
                                                                                                                                                                                  Conservative
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010; ASX_HYDROXYL; 1.
186; EGF_1; FALSE_NEG
187; EGF_CA; 1.
187; EGF_CA; 1.
187; Cytokine; Repeat; BG; Cytokine; Repeat; BG; Cytokine; Repeat; BG; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA16313.1;
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                                                                                                                                                                                                                         AA;
                                                                                         STANDARD;
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CUB; 3.
                                                                                                                                                                                                                                   80673
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ZINC (CATALYTIC) (
ZINC (CATALYTIC) (
ZINC (CATALYTIC)
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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Pred.
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CUB 2.
EGF-LIKE,
CUB 3.
                                                                                                                                                                                                                                                                                                                                                                                               BONE MORPHOGENETIC METALLOPROTEASE.
                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                         1B6980D716DC9B8D
                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bone;
; Zinc;
                                                                                                                                                                                           67;
                                                                                         639
                                                                                                                                                                                                                                                    GLCNAC.
                                                                                                                                                                                                                                 (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Cartilage;
; Calcium; §
                                                                                                                                                                                                                                                                                                                                                                 CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                        DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as its content
                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                (BY
                                                                                                                                                                                                                                                                                                                                              (BY
                                                                                                                                                                                                   Length 707;
         Strongylocentrotidae;
                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                signal;
                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase;
                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                  (POTENTIAL)
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                                      (SUBMP)
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                                                                                                                                                                                Gaps
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CCCCCCCCRTTAXCOX
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                                                                          Query Match
Best Local
                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01400; Astacin; 1.
PRINTS; PR00480; ASTACIN.
SMART; SM00042; CUB; 2.
SMART; SM00179; EGF_CA; 1.
SMART; SM00235; ZnMG; 1.
                                                                                   DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
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CARBOHYD
                                                                                                                                                                                                                                                                                                                        PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00002; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The European Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way nodified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hwang S.P.L., Partin J.S., Lennarz W.J.;
"Characterization of a homolog of human bone morphogenetic in the embryo of the sea urchin, Strongylocentrotus purpura Development 120:559-568(1994).

--- TISSUE SPECIFICITY: ECTODERMAL AND PRIMARY MESENCHYM CE
                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L23838;
HSSP; P00736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                        METAL
                                                                                                                                                                                               ACT_SITE
                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                      Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; M12.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94215496; PubMed=8162855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7668;
[1]
                                                                                                                                                                                                                                                                                 ROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [nterPro;
                                                                                                                                                                                                                                                                                                        fetalloprotease; EGF-like domain;
  73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE: EMBRYO; HIGHEST LEVEL SIMILARITY: BELONGS TO PEPTIDASE FAMILY MISSIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN. SIMILARITY: CONTAINS 2 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HATCHED BLASTULA.
GRLASPGFPGEYANDQERRWTLTAPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00008; EGF; PF00431; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o; IPR001506; Astacin.
c; IPR000152; Asx_hydroxyl.
c; IPR000859; CUB_domain.
c; IPR000561; EGF_like.
c; IPR001881; EGF_Ca.
c; IPR000130; Zn_MTpeptdse.
                                   Similarity
                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA30081.1; -.
                                                                                                                                                                                                                                                                                                                     protein;
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                                                                        3
                                                                    455 N
71893 MW;
                                                                                                 27.7%;
40.7%;
                                                                                                                                                                                                                                                                                                                  Repeat; Hydrolase; Protease;
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                                                                                                                               EGF-LIKE, CALCIUM-
ZINC (CATALYTIC) (
BY SIMILARITY,
ZINC (CATALYTIC) (
ZINC (CATALYTIC) (
ZINC (CATALYTIC) (
BY SIMILARITY,
BY SIMILARITY,
BY SIMILARITY,
BY SIMILARITY,
                                  Score 66;
Pred. No.
                                                                                   N-LINKED
N-LINKED
                                                                                                                                                                                                                                          BONE MORPHOGENETIC METALLOPROTEASE.
CUB 1.
                                                                                                                      N-LINKED
                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                      593078265B7894AD
                      Mismatches
                                                                                                                                                                                                                                                                                                        Calcium;
                                                                                   O (GLCNAC. . .)
O (GLCNAC. . .)
O (GLCNAC. . .)
O (GLCNAC. . .)
                                                                                                                                                                                                        CALCIUM-BINDING (POTENTIAL).
ALYTIC) (BY SIMILARITY).
                                             DB
                                               <u>ب</u>
                                                                                                                                                                                                                                                                                                        Signal
                                                                                                                                                                    (BY
                                             Length 639;
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                                                                       CRC64;
                                                                                                                                                                                                                                                                   PROTEIN 1 HOMOLOG
                                                                                                                                                                    SIMILARITY)
SIMILARITY)
                      Indels
                                                                                           ) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                  Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purpuratus
                                                                                   (POTENTIAL)
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RESULT 17
NRP1_CHICK
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PROSTIL
Transmembra.
Cell adhesion 1
TGNAL 19
20
                                                                                                     PRINTS; PRO0020; MAMDOMÁIN.
SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01186; FA58C_1; 2
PROSITE; PS01286; FA58C_2; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRP1_CHICK P79795;
                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC (LAYERS D AND E OF SGFS), AMACRINE CELLS OF RETINA, DORSAL ROOT GANGLIA, ALSO EXPRESSED IN NONNEURONAL (BLOOD VESSELS IN THE ENTIRE EMBRYO.
-!- SIMILARITY: BELONGS TO THE NEUROPILLN FAMILY.
-!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 developing chick nervous system.";

Dev. Biol. 170:207-222(1995).

-i- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE

CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF

CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERV

SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS

SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, I
16-OCT-2001 (Rel. 40, I
Neuropilin-1 precursor
                                                                                                                                                                                                                                                                                                EMBL; D45416; BAA08256.1; -. HSSP; P12259; 1CZT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-White leghorn; TISSUE-Embryonic brain; MEDLINE-95324761; PubMed-7601310; Takagi S., Kasuya Y., Shimizu M., Matsuura T.
                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                    InterPro; IPR000859; CUB_domain
InterPro; IPR000421; FA58_C.
                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Expression of a cell adhesion molecule, neuropilin,
developing chick nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRP1 OR NRP
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                                                                            PROSITE; PS00740; MAM_1; PROSITE; PS50060; MAM_2;
                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                         entities requires a
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PF00754; F5_F8_type_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000421;
IPR000998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 35, Creater, (Rel. 35, Last sequence update, (Rel. 40, Last annotation update)
                                                              Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
      18
914
847
                                                                                                                                                                                                                                                                                                                                                      license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                      MAM_domain
                                                                                                        22
                                                              Neurone; Signal; Repeat; Receptor;
    POTENTIAL.
NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                      for commercial
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DO COLDA1
OS GALLUS
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                                                                                                                                                                                                                                                                                                                                                                                 "Cartilage type amino-terminal gi
J. Biol. Chem. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COL9A1.

Gallus gallus (Chicken).

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; C

Eukaryota; Aves; Neognathae;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·Collagen alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P12106;
01-OCT-1989
                                                                                                                                                                                                                                                     Proc.
                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 417-504 FROM N.A. MEDLINE=85216631; PubMed=3858862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-299 FROM N.A., AND PARTIAL SEQUENCE MEDLINE-88115376; Pubmed-3339014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-416 FROM N.A. MEDLINE-90062114; PubMed-2584206;
                                                                                                                                                                                                                                                                                                      Lozano G., Ninomiya Y., Thompson H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              asios G., Nishimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                   collagen polypeptides.
oc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                                                    distinct class of vertebrate collagen genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
                                                                   3(IX) chain.

DOMAIN: EACH SUBUNIT IS COMPOSED OF THREE TRIPLE-HELICAL DOMAINS INTERSPERSED WITH NONCOLLAGENOUS DOMAINS. THE GLOBULAR DOMAIN AT THE N-TERMINUS OF TYPE IX COLLAGEN MOLECULES REPRESENTS THE NC4 DOMAIN WHICH MAY PARTICIPATE IN ELECTROSTATIC INTERACTIONS WITH POLYANIONIC GLYCOSAMINOGLYCANS IN CARTILAGE.
                                   PTM: Covalently linked to the telopeptides lysine-derived cross-links.
                                                                                                                                                                                                         of the eye.
                                                                                                                                                                                                                                 FUNCTION: Structural
                                                                                                                                                                                         SUBUNIT: Heterotrimer of a alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYLTSPGYPQSYHPSQKCEWLIQAPEPYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                              B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Similarity
12; Conser
PROLINES AT THE THIRD POSITI (G-X-Y) ARE HYDROXYLATED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 26, Last sequence up
(Rel. 32, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                   globular domain enco
263:2324-2329(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1(IX) chain precursor (Fragments).
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                   THE THIRD POSITION
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                                                                                                                                                                                                                                                   S.A.
                                                                                                                                                                                                                               component
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Konomi
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PROBABLE.
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                                                                                                                                                                                                                                                 82:4050-4054(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vert; Galliformes;
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SIMILARITY.
DD2EE6D6F0CBB68C CRC64;
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                   OF THE
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Phasianidae; Phasianinae;
ALL
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RESULT 19
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Best Local
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P25723; O9VC46;
01-MAY-1992 (Rel. 2
01-MAY-1992 (Rel. 2
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                              01-MAY-1992 (Rel. 22, Created)
16-CCT-2001 (Rel. 40, Last annotation update)
Dorsal-ventral patterning tolloid protein pred
TLD OR CG6868.
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DISULFID
CONFLICT
CONFLICT
SEQUENCE
                                                                                 SEQUENCE FROM N.A.
STRAIN=Canton-S;
MEDILINE=92034970; PubMed=1840509;
Shimell M.J., Ferguson E.L., Childs S.R.,
"The Drosophila dorsal-ventral patterning human bone morphogenetic protein 1.";
                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Bracl
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
           2]
SEQUENCE FROM N.A.
MEDLINE=95324373; PubMed=7600963;
Finelli A.L., Bossie C.A., Xie T.,
Finelli A. T., analysis of the Drosop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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EMBL; J03539;
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or send an email to license@isb-sib.ch).
Development 120:861-870(1994).
       nomolog ";
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                                                                          67:469-481(1991).
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A28754; A28754.
B34493; B34493.
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; J03539; AAA48702.1;
; M11325; AAA48642.1;
; M11324; AAA48642.1;
                                                                                                                                                                                                                                                                                                                                         PPGPPGPDGDAGKAGSPGLPGEPGAD-----GLTGPDG
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ro; IPR001791; Laminin_G.
ro; IPR003129; TSPN.
SM00210; TSPN; 1.
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Pred. No. 1.8;
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ION (N-TERMINAL) (NC4).
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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Balew R.M., Basun A., Berman B.P., Bhandari D., Bolshakov S., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Y., Mays A.D., Dew I., Dietz S.M., Dowlos M., Dowlos M., Dowlos M., Dowlos M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dorbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N. S., Gelbart W. M., Glasser K., Dunn P., Colser C., Gabrielian A.E., Garg N. S., Gelbart W. M., Glasser K., Dunn P., Borris M., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Harvey D., Heiman T.J., Hernandez J.R., Kulp D., Lai Z., Lai Z
                                            FlyBase; FBgn0003719; tld.
InterPro; IPR001506; Astacin.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF_like.
InterPro; IPR0001881; EGF_Ca.
InterPro; IPR000130; Zn_MTpeptdse.
InterPro; IPRO00
InterPro; IPRO00
InterPro; IPRO00
InterPro; IPRO00
Pfam; PF00008; I
                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                     EMBL; M76976; AAA28491.1; -. EMBL; U04239; AAC46482.1; -. EMBL; AE003749; AAF56329.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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MEDLINE-20196006; PubMed-10731132;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                    MEROPS; M12.010;
                                                                                                                                                                                                                                           HSSP; P00742;
                                                                                                                                                                                                                                                              PIR; A39288; A39288.
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SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHYSICALLY WITH DPP-C PROTEIN
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RESULT 20

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PROSITE; PS001100; CUB; 5.
PROSITE; PS001010; ASX_HYDROXYL; 2.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_GA; 2.
Developmental protein; Hydrolase; Met
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SMART; SM00179; EGF_CA; 2.
SMART; SM00235; ZnMC; 1.
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SMART; SM00231; FA58C; 2:
SMART; SM00137; MAM; 1:
PROSITE; PS01180; CUB; 2:
PROSITE; PS01285; FA58C_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IF FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
SUBCELLULAR LOCATION: Type I membrane protein.
ITSSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE LINING IN THE RIBS.
INVING IN THE RIBS.
SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
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STRAIN-Sprague-Dawley;
MEDLINE=97433085; PubMed=9288754;
Kolodkin A.L., Levengood D.V., Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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Pfam;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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PF00754; F5_F8_type_C;
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CUB 2
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                              TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
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11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT: *
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363	AAY244/3	AAW56151	AAW19720	AAM93217	AAB75322	AAU00198	AAII00190	AAU00713	AAUUU2U6	AAU00210	AAU00199	AAU00191	AAU00195	AAU00207	AAU00719	AAU00712	AAU00201	AAU00193	AAU00197	AAU00209	AAU00714	AAU00200	AAU00192	AAU00196	AAUUU2U8	AAU00713	AAG80757	ABB50288	AAU84299	AAWU/609	ABB61958	AAE15860	AAU81976	AAB70538	AAE15853	AAE15854	AAB70542	054	7054	85	850	AAR47559
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ALIGNMENTS

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DT 17-1
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KW Hume
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XX AAE14563; AAE14563 standard; peptide;

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Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion; human immunodeficiency virus; pathogenic bacteria; inflammatory disorder.

Human 20 kDa MASP-2 fragment

17-MAY-2002

(first entry)

Homo sapiens

WO200206460-A2

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Matches 41
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                                                                                                                                                                                        Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion; human immunodeficiency virus; pathogenic bacteria; inflammatory disorder
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01-JUN-2001; 2001DK-0000870.
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AAE14565 standard; peptide; 671
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                                                                           Location/Qualifiers
15..671
/note= "This region is specifically claimed claim 45"
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                                            Region
                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion;
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                                                                                                                                                                                                                                                                                                       Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunodeficiency virus; pathogenic bacteria;
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16..31
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16..56
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"This region is specifically claimed in claim
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Pred. No. 5.4e-22;
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                                                                                                                   The invention relates to use of a polypeptide derived from mannan-binding lectin (MBL) associated serine protease-2 (MASP-2) for producing a pharmaceutical composition. MASP-2 is a complement-fixing enzyme and involved in lectin pathway of complement activation. The pharmaceutical composition comprising MASP-2 is useful for treating infections caused by microbes such as fungus, yeast, and the pharmaceuticum caused by microbes such as fungus, yeast, and the pharmaceuticum caused by microbes such as fungus, yeast, and the pharmaceuticum caused by microbes such as fungus, yeast, and the pharmaceuticum caused by microbes such as fungus, yeast, and the pharmaceuticum caused by microbes such as fungus, yeast, and the pharmaceuticum caused by microbes such as fungus, yeast, and the pharmaceuticum caused by microbes such as functions.
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01-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (JENS/) JENSENIUS J C. (THIE/) THIEL S.
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                                                                                                                                                                                                                                       76pp;
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/note= "Complement
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RESULT 4
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Best Local :
                                                                                                                                                 Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for producing pharmaceutical composition, to treat bacterial, fungal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders. The present sequence is human MASP-2 protein. Note: The present sequence is stated as being the same as SEQ ID NO:2 shown in sequence listing of the specification However the sequences differ at various locations.
                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUL-2000; 2000DK-0001089
01-JUN-2001; 2001DK-0000870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human MASP-2 protein, alternative version.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAY-2002
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                                                                                                                                                                                                                                                                                                                    Jensenius JC,
                                                                                                                                                                                                                                                                                                                                                               (JENS/) JENSENIUS J
(THIE/) THIEL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUL-2001; 2001WO-DK00499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunodeficiency virus; pathogenic bacteria; inflammatory disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mannan-binding lectin associated serine protease-2; MASP-2; MBL;
                                                                                                                                                                                                                                                   AAD24224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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299
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16..686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Encoded by
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No. 5.5e-22;
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The invention relates to use of a polypeptide derived from mannan-binding lectin (MBL) associated serine protease-2 (producing a pharmaceutical composition. MASP-2 is a complementation of the composition of the complementation of the composition of the composi

(MASP-2)

for

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                                                                                                                                                                                     diagnostics, foreusacc, responsible for genetic
polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                  The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                           Claim 20;
                                                                                                                                                                                                                                                                                                                                    Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders. The present sequence is human MASP-2 protein. Note: The present sequence is stated as being the same as SEQ ID NO:2 shown in figure 6 of the specification (AAE14564). However the sequences differ at various locations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          retrovirus (e.g. human immunodeficiency virus (HIV)), or pathogenic bacteria which are resistant to at least one antibiotic medicament or multiresistant. The polynocleotide encoding MASP-2 is useful for treating patients deficient in MASP-2. The invention also discloses MASP-2 assays which are useful for determination of MASP-2 activity or levels in patients suffering from e.g. infections, inflammatory disorders and spontaneous recurrent abortion. The pharmaceutical composition Composising MASP-2 inhibitor is useful for treating inflammatory
                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                  N-PSDB; AAS85321
                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-0540217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG21134 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human diagnostic protein #21125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating infections caused by microbes such as fungus, yeast
                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ing enzyme and involved in lectin pathway of complement pharmaceutical composition comprising MASP-2 is useful
                                                                                                                                                                                                                                                                                                    2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                          SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                        51493; 103pp;
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Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
.5e-22;
s 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder
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                                                                                                                                                                                                                              mutations
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RESULT 6
AAU87257
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Best Local
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07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostics forensics gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                         18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                      16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                       24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenocarcinoma; reproductive system disorder; testicular feminisatio endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney fallure; blood disorder myocardial infarction; wound healing; cell prolliferation; skin aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Central nervous system; CNS; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                       04-FEB-2000
                                                                                                                                                                                                                                                                                    31-JAN-2000;
                                                                                                                                                                                                                                                                                                                   17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quantitating a polypeptide in tissue,
                                                                                                                                                                                                                                                                                                                                                                               WO200155318-A2
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel central nervous system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       food supplement. (II) and its binding partners are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                            additive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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2000US-0209467.
2000US-0214886.
2000US-0215135.
2000US-0216647.
2000US-0216647.
2000US-0217487.
2000US-0217487.
2000US-0217496.
2000US-021963.
2000US-0220964.
2000US-0220964.
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2000US-0205515
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2000US-0190076.
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2000US-0186350
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2000US-0180628
                                                                                                                                                                                                                                                                                                                   2001WO-US01332
                                                                                                                                                                                                                                                                                                                                                                                                                                          tood preservative; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein #167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 238; DB 22; Pred. No. 8.7e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        testicular teminisation
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2000US-022451 2000US-022521

2000US-0225268. 2000US-0225270. 2000US-0225447. 2000US-0225757. 2000US-0225758. 2000US-0225759. 2000US-0226279.

2-AUG-2000; 3-AUG-2000;

2000US-0226681. 2000US-0226868. 2000US-0227182. 2000US-0227009.

2000US-0228924. 2000US-0229287. 2000US-0229343. 2000US-0229344.

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The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative clisorders e.g. neoplasms of the breast or liver, cardiovascular disorders c.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemila, angiogenesis, nervous system disorders e.g. Alpheimer's disease and camplotrophic lateral sclerosis, infections caused by bacteria, viruses c.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders c.g. carenomas and irritable bowel syndrome, reproductive system consideration, cancers and disorders e.g. dysphagia, cancers e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g.
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17-NOV-2000
17-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid encoding a preventing, treating or ameliorating food additives or preservatives -
                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen
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8-NOV-2000;
8-NOV-2000;
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DB; ABK43587.
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2-2000;
2-2000;
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                                                                                                                                                                                                                                                                                                                      SEQ
disorders involving
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2000US-0251869.
2000US-0251989.
2000US-0251990.
2000US-0254097.
2001US-0259678.
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2000US-0256719.
2000US-0251479.
2000US-0251856.
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2000US-0249215.
2000US-0249216.
2000US-0249217.
2000US-0249218.
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2000US-0246525.

2000US-0246526.

2000US-0246527.

2000US-0246528.

2000US-0246532.

2000US-0246609.

2000US-0246610.

2000US-0246611.

2000US-0246613.

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2000US-0246613.
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2000US-0249209.
2000US-0249210.
2000US-0249211.
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2000US-0246523
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2000US-0249245
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2000US-0249213
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  neovascularisation
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                                                                                                                                                                                                                                                                                                                                                                           medical
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9
  malignancies,
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05-SEP-2000 05-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000

2000US-0230437. 2000US-0230438. 2000US-0231242. 2000US-0231243.

2000US-0229509 2000US-0229513

2000US-0236369 2000US-023670 2000US-0237037 2000US-0237037 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0239937 2000US-0241786 2000US-0241786 2000US-0241786 2000US-0241786 2000US-0241786 2000US-0241786 2000US-0241786 2000US-0241786 2000US-0241786 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241809 2000US-02446475 2000US-02446174 2000US-02446175 2000US-02446475

27 SEP 2000 29 SEP 2000 20 CCT 2000 02 CCT 2000 02 CCT 2000 03 CCT 2000 04 CCT 2000 05 CCT 2000 07 CCT 2000 07 CCT 2000 08 CCT 2000 09 CCT 2000 01 CCT 2000 01 CCT 2000 02 CCT 2000 03 CCT 2000 04 CCT 2000 05 CCT 2000 06 CCT 2000 07 CCT 2000 08 CCT 2000 09 CCT 2000 00 CCT 2000 00 CCT 2000 01 CCT 2000 01 CCT 2000 01 CCT 2000 02 CCT 2000 03 CCT 2000 04 CCT 2000 06 CCT 2000 07 CCT 2000 08 CCT 2000 09 CCT 2000 00 CCT 2000 01 CC

2000US-0235834. 2000US-0235836. 2000US-0236327. 2000US-0236367.

2000US-0236368

2000US-0234223. 2000US-0234274. 2000US-0234997.

2000US-0232399 2000US-0232400 2000US-0232401 2000US-0233063 2000US-0233064 2000US-0233064

2000US-0234998 2000US-0235484

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Best Loc
Matches
    11-JUL-2000

14-JUL-2000

14-JUL-2000

26-JUL-2000

26-JUL-2000

14-AUG-2000

14-AUG-2000
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19-MAY-2000;
77-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal dipulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation.
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21; Conservative
    2000US - 198123P

2000US - 205515P

2000US - 214886P

2000US - 214886P

2000US - 2151345P

2000US - 215880P

2000US - 21748PP

2000US - 217496P

2000US - 217496P

2000US - 217496P

2000US - 220964P

2000US - 220964P

2000US - 224518P

2000US - 225214P

2000US - 225218P

2000US - 225219P

2000US - 22
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Pred. No. 0.00039;
3; Mismatches 13;
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    14-SEP 2000
11-SEP 2000
21-SEP 2000
25-SEP 2000
25-SEP 2000
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29-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
20-OCT 2000
02-OCT 2000
03-OCT 2000
03-OCT 2000
04-NOV 2000
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08-NOV 2000
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22-AUG-2000
23-AUG-2000
30-AUG-2000
01-SEP-2000
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05-SEP-2000
06-SEP-2000
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2000US-232401P.
2000US-233063P.
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2000US - 23423P

2000US - 234274P

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2000US - 235834P

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2000US - 235836P

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2000US-229513P.
2000US-230437P.
2000US-230438P.
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2000US-227182P.
2000US-227009P.
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RESULT 8
AAU19914
ID AAU1
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AC AAU1
AC AAU1
XX
DT 06-E
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DE NOVE
XX
Huma
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Best Local 9
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, nuscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                   renal
is a p
                                                                                                                                                                                                                                                                                                                                                 Sequence
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      Human;
                                     Novel human
                                                                     06-DEC-2001
                                                                                                       AAU19914;
                                                                                                                                   AAU19914 standard;
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DB; ABA06477.
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                                                                                                                                                                                                                                                                                  21;
 calcium-binding protein; calcium flux; neurological disease;
                                                                                                                                                                                                                                                                                                    Similarity
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                                   calcium-binding
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2000US -24921P

2000US -24924P

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2000US -24929P

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2000US -25939P
                                                                    (first entry)
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                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                               39.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecule encoding an inflammation-associated n preventing, treating or ameliorating a media
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                                                                                                                                      174
                                   protein #23
                                                                                                                                                                                                                                                                              Score 93.5; DB 22;
Pred. No. 0.00039;
3; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listing; English
                                                                                                                                                                                                                                                                                                               Length 174;
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                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                2;
   31-JAN-2000
04-FEB-2000
04-FEB-2000
01-MAR-2000
11-MAR-2000
11-MAR-2000
07-JUN-2000
07-JUL-2000
07-JUL
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blood disorder; infectious disease; gene therapy; immunosuppressive;
antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-2001
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2000US-0179065

2000US-0186628

2000US-01886648

2000US-01886678

2000US-019874

2000US-0198123

2000US-0198135

2000US-0216846

2000US-0216846

2000US-0211680

2000US-0211890

2000US-021890

2000US-021890

2000US-0224518

2000US-0224518

2000US-0224518

2000US-0225214

2000US-0225214

2000US-0225214

2000US-0225216

2000US-0225216

2000US-0225217

2000US-0225266

2000US-022526

2000US-0231244

2000US-0233124

2000US-0233124

2000US-0233296

2000US-02333063

2000US-02333063
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29-SEP-2000;
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29-SEP-2000;
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27-SEP-2000;
27-SEP-2000;
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2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251869.
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2000US-0249211.
2000US-0249213.
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2000US-0249214.
2000US-0249215.
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2000US-0236327.
2000US-0236367.
2000US-0236368.
2000US-0236368.
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2000US-0249217
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2000US-0239935
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2000US-0236802
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2000US-0249265
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2000US-0246477
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AAG01729
     DT NOS X W X E X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X P X X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X
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11-DEC-2000;
05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represent the novel human calcium binding proteins. Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). In novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amylotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel human calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases
                          Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activities mediated by calcium-binding proteins. The polynucleotides the invention are also useful in gene therapy. AAU19892-AAU19969
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N-PSDB; AAS31599.
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                                                                                                                                                                                                                                                                                                                                                                            gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                        Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG01729 standard;
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                                                                        (GEST ) GENSET.
                                                                                                                          26-FEB-1999;
                                                                                                                                                                                                                                                                                                                          Homo sapiens
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nilarity 40.4%;
Conservative
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2000US-0254097.
2001US-0259678.
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                                                                                                                                                                                                                                                                                                                                                                              chromosome mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                   expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein, SEQ ID NO: 5810
                                                                                                                            99US-0122487
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Pred. No. 0.00039;
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Best Local
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                                                                                            New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedure
The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30
                                                                     Claim 13;
                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                 Dumas Milne Edwards
                                                                                                                                                                                                                                                                                  26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                    (GEST ) GENSET
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                                                                                                                                                                   2000-500381/45.
DB; AAC00227.
                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy;
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DB; AAC01735.
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                                                                  71pp + CD-ROM;
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                                                                                               mapping procedures
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RESULT 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; protease; PRTS; gastrointestinal disorder; peptic esophagitis; indigestion; gastritis; cardiovascular disorder; reproductive disorder; hypertensive heart disease; myocardial infarction; autoimmune disorder; inflammatory disorder; rheumatoid arthritis; cell proliferative disorder; arteriosclerosis; cancer; epithelial disorder; eczema; endometriosis;
                                                                                     Modified-site
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45.2%;
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               Potential
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Pred. No.
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Modified-site

Potential

phosphorylation site

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17-MAR-2000;
30-MAR-2000;
14-APR-2000;
20-APR-2000;
 The
                   Claim 1;
                                   polynucleotides
                                             New polypeptide for treating gastrointestinal, autoimmune disorders, comprises novel human pr
                                                                         N-PSDB;
                                                                                                     Hafalia A,
                                                                                                           Yue H, Lu DAM, Policky JL,
Au-Young J, Bandman O, Lal
Tang YT, Burford N, Baughn
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sequences
                                                                         2001-611509/70
DB; AAH43512.
                                                                                                                                                  INCYTE GENOMICS
                  Page 109-11;
                                                                                                                                                                   ; 2000US-190708P.
; 2000US-193182P.
; 2000US-197086P.
; 2000US-199022P.
; 2000US-200227P.
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                129pp; English.
AAB47559-69 show novel human proteases PRTS-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease active site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential glycosylation site
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                                                                                                                                Delegeane AM,
                                                                                                                                                                                                                                                                                                                      protease
                                                                                                            Borowsky ML,
Nguyen DB,
                                                                                                                                                                                                                                                                                                                                                         glycosylation site
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                                             proteases
                                                                                                                             Tribouley CM,
                                                                                                             Gandhi AR, Hi
Yao MG, Walia
                                           cardiovascular and oteases (PRTS) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       site
                                                                                                                     Hillman
                                                                                                                                Khan FA;
                                                                                                             NK,
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Ϊ'n

The invention relates to a mannan-binding lectin (MBL) associated serine protease-3 (MASP-3) polypeptide. MASP-3 exerts an inhibitory effect on the complement activation particularly when bound to MBL/MASP-2 complexes and directly activates complement system through binding to MBL. The MASP-3 polypeptides, polynucleotides and modulators are useful for preparing a pharmaceutical composition for treating aberrant MASP-3 activity such as infections, cancer, MBL-deficiency, disorders of the

reproductive system diseases associated

associated with

cancer, MBL-deficiency, disorders of the ve system. The MASP-3 polypeptide is also ssociated with human immunodeficiency virus,

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RESULT 12
AAB85060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferative (arteriosclerosis, cancers), epithelial (eczema), neurological (Huntington's disease), and reproductive (endometriosis disorders. This protein shows homology with the human precursor of P100 serine protease of Ra-reactive factor.
                                                                                                                                Claim
                                                                                                                                                      Novel pure mannan-binding lectin associated serine protease polypeptides and polypucleotides encoding the protein, used treating reoxygenated ischemic tissues, mannon-binding lectideficiency, multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiatherosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB85060
                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                Jensenius JC,
                                                                                                                                                                                                                                                                                                                                21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                              02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                        30-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                           WO200140451-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarthritic; antianemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mannan-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mannan-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human serine protease MASP-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-2001
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                                                                                                                                                                                                                                                                                                      (JENS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wannan-binding lectin associated serine protease-3; MASP-3; MBL; mannan-binding lectin; complement; infection; cancer; cytostatic; immunomodulator; neuroprotective; anticonvulsive; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 MFGQIQSPGYPDSYPSDSEVTWNITVPDGFR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 VFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                      2001-374820/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
14; Conserv
                                                                                                                                                                                                                                                                                          JENSENIUS
THIEL S.
                                                                                                                                                                                                                           AAF83895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         These proteases can be administered in pharmaceutical compounds
                                                                                                                               Page 88-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             728 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                99DK-0001721.
2000DK-0001126.
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45.2%;
                                                                                                                              99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; antipsoriatic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide
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0.0021;
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                                                                                                                                                                     lectin
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DR PT DR XXX
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Matches 14
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medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder (e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator cactivity or of latency or predisposition to a PROX-associated disorder AAF74432 to AAF74448 encode the specifically claimed human PROX
                                                                                                                                                The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene
                                                                                                                                                                                                                                                                              Nucleic acids encoding secreted polypeptides, designated PROX polypeptides, useful for treating a syndrome associated with PROX-associated disorder, e.g. cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                      Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-AUG-1999; 99US-0148433
10-AUG-2000; 2000US-0148433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO9 protein sequence SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple sclerosis, myasthenia gravis, epilepsy, rheumatoid arthritis, vasculitis, autoimmune hemolytic anemia, Crohn's disease, asthma,
                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-147509/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-AUG-2000; 2000WO-US21857
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                                                                                                             therapy, and as PROX antagonists and PROX agonists. PROX polypeptides nucleic acids and antibodies are useful in the manufacture of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURA-) CURAGEN CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated disorder;
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Pred. No.
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RESULT 14
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                                                                            The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder (e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding secreted polypeptides, designated PROX polypeptides, useful for treating a syndrome associated with a PROX-associated disorder, e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; PRO; PROX; cytostatic; immunomodulatory; reproduction; gene therapy; cell proliferation; differentiation disorder; cimmune associated disorder; gestational disease; pre-clampsia
                                                                                                                                                                                                                                                                                        Claim 1; Page 35-37; 166pp; English.
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10-AUG-2000; 2000US-0148433
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                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF74441.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Shimkets RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
               Similarity
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 Conservative
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            38.4%;
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             Score 91.5;
Pred. No. 0
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Pred. No. 0.0023;
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pre-clampsia
Indels
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5 PKW--PEPV--

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----FGRLASPGFPGEYANDQERRWTLTAPPGYR 41

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RESULT 15
AAB70541
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                                                                                                                                      RESULT 16
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PROI to PROI7 given in AAB70531 to AAB70547.
  09-MAY-2001
                                              AAB70542;
                                                                                        AAB70542 standard; Protein; 526
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding secreted polypeptides, designated PROX polypeptides, useful for treating a syndrome associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimkets RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO11
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                                                                                                                                                                                                     403 PFWDSKEPVCIAACGGVIRNGTTGRIVSPGFPGNYSNNLTCHWLLEAPEGQR 454
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                                                                                                                                                                                                                                                                                                                                                                                     525
                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                            -FGRLASPGFPGEYANDQERRWTLTAPPGYR 41
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No. 0.
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0.0023;
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Best Local
                neurological disorder; muscular dystrophy; muscle injury; vulnerary; amyotropic lateral sclerosis; multiple sclerosis; ischaemia; diabetes;
                                                            nootropic; neuroprotective; anticonvulsant; cerebroprotective; stroke; vasotropic; neuronal growth; growth factor-mediated chemotaxis; trauma;
epilepsy; Parkinson's disease; sexual development;
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                                                                                                                                                                                                                          26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 21; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526 AA;
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medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder disorder acceptance of the disorders and a gestational disease of the disorders and a gestational disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a
Human; SEZ6; neural regeneration; seizure; infertility; gene therapy; stroke; Alzheimer's disease; Huntington's disease; myasthenia gravis;
                                                                                                       Human SEZ6 mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 41-43; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding secreted polypeptides, designated PRO polypeptides, useful for treating a syndrome associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-AUG-1999; 99US-0148433
10-AUG-2000; 2000US-0148433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROX-associated disorder, e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    403 PFWDSKEPVCIAACGGVIRNGTTGRIVSPGFPGNYSNNLTCHWLLEAPEGQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PKW--PEPV------FGRLASPGFPGEYANDQERRWTLTAPPGYR 41
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                                                                                                                                                                      (first entry)
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l proliferation;
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Pred. No. 0.00
3; Mismatches
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ion; differentiation disorder; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease. SEZ6 is useful for treating a patient suffering from a neurological disorder such as epilepsy, Alzheimer's disease, Parkinson's disease, seizure related disorder or a disorder associated with stroke. SEZ6 DNA is useful as probes for gene mapping and for detecting transcription, translation and/or expression of hSEZ6 polypeptide in human tissue. A transgenic animal is useful as an animal model in research and drug development procedures, and for testing compounds or other treatment modalities which may prevent, suppress or cure a pathology or disease associated with hSEZ6 activities. SEZ6 is also useful for treating abnormal primary or secondary sexual development, e.g., impotence, infertility or reduced libido. The hSEZ6 polynucleotide is useful for treating the above mentioned disorders by gene therapy cechniques. The present sequence is human SEZ6 mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth factor-mediated chemotaxis, altered behavioural patterns, e.g., sleep or eating disorders and for treating neurological disorders such as trigeminal neuralgia, Bell's palsy, myasthenia gravis, muscular dystrophy, muscle injury, invertebrate disk syndrome, thoracic outlet destruction syndrome, amyotropic lateral sclerosis, multiple sclerosis, ischaemia associated with stroke, neuropathy associated with diabetes, spinal cord trauma, facial nerve crush and other trauma, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human SEZ6 polypeptide useful for inducing neural regeneration, inhibiting neural degeneration, preventing seizures, and for treating infertility, Alzheimer's disease, stroke, seizures, Huntington's
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N-PSDB; AAD25344.
                                                        Human SEZ6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9;
    Human; SEZ6; neural stroke; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated human SEZ6 (hSEZ6) polypeptide and
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                                                                                                     26-MAR-2002
                                                                                                                                                                               AAE15853 standard;
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les 21; Conser
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                                                                                                                                                                                                                                                                          PFWDSKEPVCIAACGGVIRNATTGRIVSPGFPGNYSNNLTCHWLLEAPEGQR 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                      829 AA;
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                   (first
                                                                                                                                                                             Protein; 853
regeneration; seizure; infertility; gene therapy; disease; Huntington's disease; myasthenia gravis;
                                                                                                 entry)
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No. 0.
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Query Match
Best Local :
       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth factor-mediated chemotaxis, altered behavioural patterns, e.g., sleep or eating disorders and for treating neurological disorders such as trigeminal neuralgia, Bell's palsy, myasthenia gravis, muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human SE26 polypeptide useful for inducing neural regeneration, inhibiting neural degeneration, preventing seizures, and for treating infertility, Alzheimer's disease, stroke, seizures, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nootropic; neuroprotective; anticonvulsant; cerebroprotective; stroke; vasotropic; neuronal growth; growth factor-mediated chemotaxis; trauma; neurological disorder; muscular dystrophy; muscle injury; vulnerary; amyotropic lateral sclerosis; multiple sclerosis; ischaemia; diabetes; epilepsy; Parkinson's disease; sexual development; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   destruction syndrome, amyotropic lateral sclerosis, multiple sclerosis, ischaemia associated with stroke, neuropathy associated with diabetes, spinal cord trauma, facial nerve crush and other trauma, Huntington's
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                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                               useful for treating abnormal primary or secondary sexual development, e.g., impotence, infertility or reduced libido. The hSEZ6 polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 119-122; 127pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dystrophy, muscle injury, invertebrate disk syndrome, thoracic outlet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  its corresponding DNA molecule. SEZ6 is useful for enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated human SEZ6 (hSEZ6) polypeptide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIL ) LILLY & CO ELI
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                                                                                                                                                                                                          techniques. The present sequence
                                       Similarity
                                                                                                                                                                                                                                                     for treating
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       Conservative
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                                       38.4%;
                                                                                                                                                                                                                                                     the above
Score 91.5; r
Pred. No. 0.00
3; Mismatches
                                                                                                                                                                                                          is human SEZ6 protein
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RESULT 20
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Best Local
      Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide whe X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated discount and approximately approximately provided the proximately approximately provided the proximately provided the provided the proximately provided the provided the proximately provided the provided the provided the provided the proximately provided the provided the provided the provided the provided the proximately provided the proximately provided the 
                                                             Human PRO8 protein sequence SEQ ID NO:16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF714432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 24-27; 166pp; English.
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PROX; cytostatic; immunomodulatory; reproduction;
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                                                                                                                       (first entry)
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Search completed: January 11, Job time: 119 secs

2003, 10:48:09

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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding secreted polypeptides, designated PRO: polypeptides, useful for treating a syndrome associated with
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10-AUG-2000; 2000US-0148433.
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immune associated disorder; gestational disease; pre-clampsia.
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403 PIWDSKEPVCIAACGGVIRNATTGRIVSPGFPGNYSNNLTCHWLLEAPEGQR 454
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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlp
-O-/cgn2_1/USPTO_spool/US09874198/runat_10012003_092043_2562/app_query.fasta_1.199
-O-/cgn2_1/USPTO_spool/US09874198/runat_10012003_092043_2562/app_query.fasta_1.199
-DB-GenEmbl -OFMT-fastap -SUFFIX=p2n.rge -MIMMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=60
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFMT-pto -NORM=ext -HEAPSIZE=500 -MILEN=0 -MAXLEN=200000000
-USER=US09874198_eCGN_1_1_3637_@runat_10012003_092043_2562 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Listing first 60 summaries
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BLOSUM62
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238
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and is score Pred. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

## SUMMARIES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stover, C.M., Thiel, S., Thelen, M., Lynch, N.J., Volume Johnsenius, J.C. and Schwaeble, W.J.

Two constituents of the initiation complex of the mannan-binding lectin activation pathway of complement are encoded by a single
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99192764
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7 33556
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/note="alternative"
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    Schwaeble, Department of Microbiology
of Leicester, University Road, PO Box

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n, MAp19 (19kDa)"
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                                                                                                                                                                                                                                                               Submitted (10-CCT-1997) Minoru Takahashi, Fukushima Medical College, Department of Biochemistry; 1 Hikarigaoka, Fukushi Fukushima 960-12, Japan (E-mail:minolta@cc.fmu.ac.jp, Tel:81-245-48-2111, Fax:81-245-48-2111) Sequence update (13-Dec-1997).
                                                                                                                                                                                                                                                                                                                                                                                               Takahashi,M., Endo,Y., Fujita,T. and Matsushita,M. A truncated form of mannose-binding lectin-associated serine protease (MASP)-2 expressed by alternative polyadenylation is component of the lectin complement pathway

Int. Immunol. 11 (5), 859-863 (1999)
                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Takahashi,M., Matsushita,M. and Fujita,T
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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27...71
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Submitted (19-OCT-19981AW.J.
and, Immunorogy, University o
138, Leicester LEI 9HN, UK
                                                                                                                                                                                                                                                                                                                                             structural gene
J. Immunol. 162 (6), 3481-3490 (1999)
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Two constituents of the initiation complex of the mannan-binding lectin activation pathway of complement are encoded by a single
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Schwaeble, W.J.
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                                                                                                                                                                                                             sequence Y09926
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16. .573
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268 c
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                                                                                                                                                                       Jensenius, J.C. and Schwaeble, W.J.
Jensenius, J.C. and Schwaeble, W.J.
Two constituents of the initiation complex of the mannan-binding
Two constituents of the initiation complement are encoded by a single
Direct Submission
Submitted (19-OCT-1998) W.J.
and Immunology, University c
138, Leicester LEI 9HN, UK
                                                                      2 (bases 1 to schwaeble, W.J.
                                                                                                                                            J. Immunol. 162
                                                                                                                                                                                                                                Stover, C.M., Thiel, S., Thelen, M., Lynch, N.J., Vorup-Jensen, T.,
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 736)
                                                                                                                                                                                                                                                                                                                                       rectin-associated protein; mannose binding lectin-associated protein; mannose binding protein; serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                               HOSA18281 736 bp mRNA linear PRI 12-JUL-1999 Homo sapiens mRNA for mannose binding lectin-associated Serine protease-2, alternatively spliced transcript (clone phl-5).
                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    Y18281.1 GI:5459314
                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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693. .698
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61. .570
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protease-2 related protein, MAp19 (19kDA)"
/protein_id="CAB50730.1"
/db_xref="GI:5459319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease-2 related 574. .720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MRLLTLLGLLCGSVATPLGPKWPEPVFGRLASPGFPGEYANDQE RWTLTAPPGYRLRLYFTHFDLELSHLCEYDFVKLSSCAKVLATLCGOESTDTERAPG KDTFYSLGSSLDITFRSDYSNEKFFTGFEAFYAAEDIDECQVAPGEAPTCDHHCHNHL GGFYCSCRAGYVLHRNKRTCSEQSL"
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264 c 2
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protease-2 related protein, MAp19 (19kDA)"
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Matches:
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    Schwaeble, Department of Microbiology
of Leicester, University Road, PO Box

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Query Match:
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                                                REFERENCE
                                                                                                                         KEYWORDS
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                                                                                                                                                ACCESSION
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             TITLE
                                    AUTHORS
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                                                                                                                                                                                                                                    CGC 189
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1184)

Stover, C.M., Thiel, S., Thelen, M., Lynch, N.J., Vorup-Jensen, T., Jensenius, J.C. and Schwaeble, W.J.
                                                                                                                                                                        Homo
             Two
                                                                                                          lectin-associated protein; protein; mannose binding protein;
                                                                                                                                                protease-2,
Y18284
                                                                                   Homo sapiens
                                                                                                                                     Y18284.1 GI:5459320
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lectin activation pathway of complement are encoded by a single
                                                                                                Homo sapiens.
           constituents of the initiation complex of the mannan-binding
                                                                                                                                                         18284 1184 bp mRNA linear PRI 12-JUL-1999 sapiens mRNA for mannose binding lectin-associated serine ease-2, incompletely spliced primary transcript, clone phl-8.
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700. .705
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22. .579
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266 c 2
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/db_xref="taxon:9606"
/chromosome="1"
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AUTHORS
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          HSMASP2
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                                                                    Arg 41
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HSMASP2
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US-09-874-198-1 (1-41) x HOSA18284 (1-1184)
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Best Local Similarity:
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J. Immunol. 162
99192764
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Schwaeble, W.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Related sequence Y09926
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1144. .1149
/gene="MASP-2"
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protein_id="CAB50731.1"

protein_id="CAB50731.1"

/db_xref==0(1:5459321"

/translation="MRLLTLLGLLCGSVATPLGPKWPEPVFGRLASPGFPGEYANDOE

/RWTLTAPPGYELRLYETHFDLELSHLCEYDFYKLSSCAKVLATLCGQDSTDTERAPG

KDTFYSLGSSLDITFRSDYSNEKFPTGFEAFYAAEDIDECQVAPGEAPTCDHHCHNHL

GGFYCSCRAGYVLHRNKRTCSEOSL"
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protease-2 related protein, MAp19 (19kDa)"
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/gene="MASP-2"
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/clone="ph1-8"
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                                  CCAGGGGAGTATGCCAATGACCAGGAGCGGCGCTGGACCCTGACTGCACCCCCCGGCTAC
                                                                                                  ACCCCCTTAGGCCCGAAGTGGCCTGAACCTGTGTTCGGGCGCCTGGCATCCCCCGGCTTT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification and characterization of a novel protein of the human complement system, mannan-binding lectin-associated serine protease-2 (MASP-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thiel,S., Vorup-Jensen,T., Stover,C.M., Schwaeble,W., Laursen Poulsen,K., Willis,A.C., Eggleton,P., Hansen,S., Holmskov,U., Reid,K.B.M. and Jensenius,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-JUN-1996) S. Thiel, University of Aarhus, Dept. of Medical Microbiol. & Immunol., Bartholin Building, Wilhelm Meyers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H.sapiens mRNA
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGFYCSCRAGYVLHRNKRTCSALCSGQVFTQRSGELSSPEYPRPYPKLSSCTYSISLE
EGFSVILDFVESFDVETHPETLCPYDFLKIQTDREEHGPFCGKTLPHRIETKSNTVTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protease-2"
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37. .2097
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/db_xref="taxon:9606"
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Primates;
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Indels:
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HSMASP2PR
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Direct Submission
Submitted (08-DEC-1998) W.J. Schwaeble, Department of Immun and Microbiology, University of Leicester, University Road, Leicester LEI 9HN, UK
On Dec 13, 1998 this sequence version replaced gi:1929053.
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2 (bases 1 to 2455)
Thiel.S., Jensen.T.V., Stover.C.M., Schwaeble,W.:
Poulsen,K., Willis,A.C., Eggleton,P., Hansen,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (bases 1 to 2455) Schwaeble, W.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2455)
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Nature 386 (6624), 506-510 (1997)
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HOMO sapiens mRNA for MASP-2 protein.
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Location/Qualifiers
1. .2455
                                                                                                                                                                                                                                                       KOTFYSLGSSLDITFRSDYSNEKPFTGFEAFYAAEDIDECQVAPGEAPTCDHHCHNHL
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/evidence=experimental
2078. . 2455
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IGTASGWGLTQRGFLARNLMYVDIPIVDHQKCTAAYEKPPYPRGSVTANMLCAGLESG
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17. .2077
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/db_xref="taxon:9606"
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| .2455
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., Hansen,S., Holmskov,U.,
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                          Submitted (20-OCT-1999) Minoru Takahashi, Fukushima Med College, Department of Biochemistry; 1 Hikarigaoka, Fuk Fukushima 960-1295, Japan (E-mail:minolta@cc.fmu.ac.jp, Tel:81-24-548-2111(ex. 2232), Fax:81-24-548-6760)
                                                                                                                                                                                                                                                                                                                       Published Only in DataBase (1999) 2 (bases 1 to 2819) Takahashi, M. and Fujita, T.
                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 2819)
Takahashi,M. and Fujita,T.
Partial genomic structure of human
(MASP)-2 (from exon 1 to exon 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens sMAP, MASP2 genes for small MBL-associated protein, MBL-associated serine protease(MASP)-2, complete and partial cds.
                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                  location/Qualifiers
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Eukaryota; Merazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 4464)
Stover, C.M., Thiel, S., Thelen,
                                                                                                                        HOSA18286 4464 bp
Homo sapiens partial MASP-2 gene
                                                  Homo sapiens
                                                                                                    Y18286.1 GI:5459322
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/product="MBL-associated
/protein_id="BAA85659.1"
/db_xref="GI:6092073"
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|693. .1824
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protein; mannose binding protein; serine protease
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RRWTLTAPPGYRLRLYFTHFDLELSHLCEYDFVKLSSGAKVLATLCGQESTDTERAPG
KDTFYSLGSSLDITFRSDYSNEKPFTGFEAFYAAEDIDECQVAPGEAPTCDHHCHNHL
                           Craniata; Vertebrata; Catarrhini; Hominidae;
Lynch, N.J., Vorup-Jensen, T.,
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                                Hominidae;
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                                               Euteleostomi;
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REFERENCE
AUTHORS
     BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jensenius, J.C. and Schwaeble, W.J.

Two constituents of the initiation complex of the mannan-binding lectin activation pathway of complement are encoded by a single
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Schwaeble, W.J.
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J. Immunol. 162 (6), 3481-3490 (1999)
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GGFYCSCRAGYVLHRNKRTCSALCSGOVFTOBSGELSSPEYPRYPKLSSCTYSISLE
EGFSVILDFVESFDVETHPETLCPYDFLKIQTDREEHGPFCGKTLPHRIETKSNTVTI
TFVTDESGDHTGWKIHYTSTAHACPYEMAPPNGHVSPVOAKYILKDSSSIFCETGYEL
LOGHLPLKSFTAVCQKDGSWDRPMPAIVDCGPPDDLCSPSGRVEYITGPGVTTYKAVI
QYSCEETFYTHKVNDGKYVCEADGFWTSSKGEKSLPVCEPVCELSARFTGGARIYGGOK
AKPGDEPWQVLGGTTAAGALLILYDNWVLTAAHAVYEOKHDASALDIRMGTLKRLSPH
YTQAWSEAVFIHEGYTHDAGFONDIALIKLNNKVVINSNITPICLPRKEAESFWRTDD
IGTASGWGLTORGFLARNLMYVDIPIVDHOKOTAAVEKPPYFRGSVTANMLCAGLESG
                                    /note="c"
2926. .4464
/gene="MASP-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mrlltllgllcgsyatplgpkwpepyfgrlaspgfpgeyandge
RRWTLTAPPGYRLRLYFTHFDLELSHLCEYDFYKLSSGAKVLATLCGQESTDTERAPG
                                                                                                                                                                                    GGFYCSCRAGYVLHRNKRTCSEQSL"
                                                                                                                                                                                                  /translation="MRLLTLLGLLCGSVATPLGPKWPEPVFGRLASPGFPGEYANDQE
RRWTLTAPPGYRLRLYFTHFDLELSHLCEYDFVKLSSGAKVLATLCGQESTDTERAPG
KDTFYSLGSSLDTFRSDYSNEKPFTGFEAFYAAEDIDECQVAPGEAPTCDHHCHNHL
                                                                                                                                                                                                                                                         /codon_start=1
/product="MAp19 protein"
/protein_id="CAB50732.1"
/db_xref="GI:5459323"
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/gene="MASP-2"
                                                                                                                                                                                                                                                                                                                                                                                                       GKDSCRGDSGGALVFLDSETERWFVGGIVSWGSMNCGEAGQYGVYTKVINYIPWIENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="MASP-2 protein"
/protein_id="CAB50733.1"
/db_xref="GI:5459324"
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/gene="MASP-2"
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'gene="MASP-2"
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/chromosome="1"
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/gene="MASP-2"
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1 (bases 1 to 4455)
Stover,C.M., Thiels,S., Thelen,M., Lynch,N.J., Vorup-Jensen,T., Jensenius,J.C. and Schwaeble,W.J.

Two constituents of the initiation complex of the mannan-binding lectin activation pathway of complement are encoded by a single
                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (19-OCT-1998) W.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Schwaeble, W.J.
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/product="MASP-2"
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                                                                                                                                            join(1. .559,1004.
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                                                                                                                                                                         join(1. .559,2415.
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                                                                                                                                                                                                                                    /cell_type="lymphocyte"
l. .4465
                                                                                                                                                                                                                                                                                         /map="1p36.2-3"
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                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                          join(16.
                                                                                         'note="a"
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                                                                                                                                                                                                                   /gene="MASP-2"
                                                                                                                                                                                                                                                                          /clone="pgM-2B"
                                                                                                                                                                                                                                                                                                              /chromosome="1"
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                                                                                                                                                                   AF321558
                                                                                                                                                                          4900 bp DNA linear PRI 18-JAN-2001 Homo.sapiens MBL-associated serine protease 2 (MASP2) gene, exons 1 through 6; and MBL-associated protein MAp19 (MASP2) gene, complete cds, alternatively spliced.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4900)
                                                         Homo sapiens
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/gene="MASP-2"
/note="d"
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LQGHLPLKSFTAVCQKDGSWDRPMPATDCGPDDDLCSPSGRVEYITGPGVTTYKAVI
QYSCEETFYTMKVNDGKYVCEADGFWTSKGSKSLPVCEPGCLSARTTGGRIKRISPH
AKPGDFPWQVLGGTTAAGALLILYDNWVLTAAHAVYEQKHDASALDIRMGTLKRISPH
YTQAWSEAVFIHEGYTHDAGFDNDIALIKLNNKVVINSNITPICLPRKEAESFMETDD
IGTASGWGLTQRGFLARNLMYVDIPIUDHQKCTAAYEKPPYPRGSVTANMLCAGLESG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="MAp19"
/protein_id="CAB50734.1"
/db_xref="GI:5459326"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mrLLTLLGLLCGSVATPLGPKWPEPVFGRLASPGFPGEYANDQE
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                                                                      21
Arg 41
                                           CCAGGGGAGTATGCCAATGACCAGGAGCGGCGCTGGACCTGACTGCACCCCCGGCTAC
                                                           ProGlyGluTyrAlaAsnAspGlnGluArgArgTrpThrLeuThrAlaProProGlyTyr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-NOV-2000) Genetic Engineering, Kyung Hee University, 1 Seochun-Ri, Kiheung-Up, Yongin City, Kyungki-Do 449-701, Korea Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 4900)
Park,D., Kim,B., Bae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Park,D., Kim,B., Baek,K. and Yoon,J. Structure of Human MASP-2 Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MRLITLLGLLCGSVATPLGPKWPEPVFGRLASPGFPGEYANDQE RRWTLTAPPGYRLRLYFTHFDLELSHLCEYDFVKLSSGAKVLATLCGQESTDTERAPG KDTFYSIGSSLDITFRSDYSNEKPFTGFEAFYAAEDIDECQVAPGEAPTCDHHCHNHL GGFYCSCRAGYVLHRNKRTCSEQSL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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join(1. .172,254. .482,639.
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL: Sw: SWISSPROT: Tr:, TREMBL: Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/Celegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Gronn Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. This sequence is the entire insert of clone RP4-635818 The true left end of clone RP4-576K7 is at 5257 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl
http://www.sanger.ac.uk/HGP/Chrl
RP4-635E18 is from the library RPCI-4 constructed by the group Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 15, 2002 this sequence version replaced gi:11967852.
During sequence assembly data is compared from overlapping clones
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                   /note="Single clone region. Assembly confirmed by restriction digest data. Single read sequenced with dGTP" 37125. .37470
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                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-4"
2691. .3057
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/db_xref="taxon:9606"
/chromosome="1"
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overlapping clone dJ576K7
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Stover.C.M., Thiel.S., Lynch,N.J. and Schwaeble,W.J.
The rat and mouse homologues of MASP-2 and MAp19, components of the lectin activation pathway of complement
J. Immunol. 163 (12), 6848-6859 (1999)
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Direct Submission
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/codon_start=1
/product="mouse MAp19"
/protein_id="CAB63701.1"
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                         /gene="MASP-2/MAp19"
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                                                                                     Submitted (13-JUL-1999) W.J. Schwaeble, Department of Immunology, University of Leicester, University Road,, Leicester LE1 9HN, UK Location/Qualifiers
                                                                                                                                                                                                                                                 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;

1 (bases 1 to 817)

Tynch N.J. and Schwaeble, W.J.
                                                                                                                                  Direct
                                                                                                                                              2 (bases 1 to 817)
Schwaeble, W.J.
                                                                                                                                                                                                      Stover, C.M., Thiel, S., Lynch, N.J. and Schwaeble, W.J.
The rat and mouse homologues of MASP-2 and MAp19, components
lectin activation pathway of complement
J. Immunol. 163 (12), 6848-6859 (1999)
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/db_xref="taxon:10090"
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nnose binding lectin-associated serine
in, MAP19 (19kDa):
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MMU19163
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                                                                                                                                                                           1 (bases 1 to 1145)
Stover, C.M., Thiel, S., Lynch, N.J. and Schwaeble, W.J.
The rat and mouse homologues of MASP-2 and MAp19, cc
lectin activation pathway of complement
J. Immunol. 163 (12), 6848-6859 (1999)
                                                                         Submitted (13-JUL-1999) W.J. Schwaeble, University of Leicester, University Roa
                                                                                                                                                                                                                                                                                                                                                      Mus musculus partial mRNA for mannose binding serine protease-2 (MASP-2 gene).
                                                                                                      Direct Submission
                                                                                                                  2 (bases 1 to 1145)
Schwaeble, W.J.
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                 Mus musculus
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/gene="MAp19"
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648. .817
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/organism="Mus musculus"
/strain="B6CBAF1/J"
/db_xref="taxon:10090"
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EQAPGNDTFYSLGPSLKVTFHSDYSNEKPFTGFEAFYAAEDVDECRVSLGDSVPCDHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="MAp19"
75. .647
                                                        Location/Qualifiers
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/db_xref="GI:6688727"
/translation="MSLPCPQLLIFLGLLWSLVATLLGSKWPEPVFGRLVSPGFPEKY
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E1 9HN, UK
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                                                               AUTHORS
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                                                                                                                                                                                                                               AB009459 AB009459.1 GI:3928516 mannose-binding lectin associated serine protease-2. Mus musculu (strain:BALB/c) 8 weeks liver cDNA to m
                       Submitted (04-DEC-1997) Minoru Takahashi, Fukushima Medical College, Department of Blochemistry: 1 Hikarigaoka, Fukushir Fukushima 960-1295, Japan (E-mail:minolta@cc.fmu.ac.jp, Tel:81-24-548-2111, Fax:81-24-548-6760)
                                                                                                                                                 Matsushita, M., Nonaka, M. and Fu
Two lineages of mannose-binding
                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                         Mus musculus Masp-2
serine protease-2,
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Mus musculus
                                                                          Direct Submission
                                                                                     Takahashi, M., Fujita, T.,
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                                                                                                                                       (MASP) in vertebrates
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/db_xref="GI:6688733"
/db_xref="GI:6688733"
/translation="MSLDCPQLLIFLGLLWSLVATLLGSKWPEPVFGRLVSPGFPEKY ALTONGENTAPPGYBLRLYFTHFDLELSYRCEYDFVKLSSGTKVLATLCGQESTDT EQAPGNDTFYSLGPSLKVTFHSDYSNEKFTTGFEPYAABDVDECRVSLGDSVPCDHY CHWYLGGYVCSCRAGYVLHONKHFYCSALCSGQVETGKSCYLSSPBYPOPYPKLSCTY SIRLBGFSVILDFVESEDVETHPEAQCPYDSLKIQTDKGEHGPECGKTLPPRIETDS HKVTITFATDESGNHTGWKIHYTSTARPCDDTAPPNGSISPVQAIYVLKDRFYVFCK TGFELLOGSVPLKSFTAVCQKDGSWDRFMPECS"
45..104
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ca, M., Nonaka, M. and Fujita,
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protease-2"
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/codon_start=1
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                          3070 bp mRNA linear RC Mus musculus, Similar to mannan-binding lectin serine clone MGC:13718 IMAGE:4211293, mRNA, complete cds. BC013893.1 GI:15530224
                                                            Direct Submission
Submitted (07-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 3070)
                                                                                                                                                             Strausberg, R.
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DGFSYILDFYESEDHOETHPEAGCFYDSLKIQTDKGEHGPFCGKTLPPRLETDSHKVTI
TFATDESGHITGWKLHYTSTARPCPDDTAPPNGSISPYOATYVLKDRFSVECKTGFEL
LQGSVPLKSFTAYCQKDGSMDRPMPECSIIDCGPPDDLPNGHVDYITGPOVTTYKAVI
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RSWTLTAPPGYRLRLYFTHFDLELSYRCEYDFVKLSSGTKVLATLCGQESTDTEQAPG
NDTFYSLGPSLKVTFHSDYSNEKPFTGFEAFYAAEDVDECRVSLGDSVPCDHYCHNYL
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KPGDFPWQVLLLGQTTAAAGALIHDNWYLTAAHAVYEKRMAASSLNIRMGILKRLSPH
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/strain="BALB/c"
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KDSCRGDSGGALVFLDNETQRWFVGGIVSWGSINCGAAGQYGVYTKVINYIPWNENII
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33. .2090
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/db_xref="GI:3928517"
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/tissue_type="liver"
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RESULT 18
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                                                                                                                                                       Arg 41
Mouse DNA sequence from clone RP22-211A10 on chromosome 4, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Series: IRAK Plate: 18 Row: n Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 675.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                         AL591032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.systemsbiology.org
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DGFSVLLDFVESFDVETHPEAGCPYDSLK1QTDKGEHGFFCKKTLPFRIETDSHKVTI
TFATDESGNHTGMKHYTSTARPCPDDTAPPNGSISPVALIYYLKDRFSVFCKTGFEL
LQGSVPLKSFTAVCQKDGSWDRPMPECSIIDCGPPDDLPNGHVDYITGPEVTTYKAVI
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KPGDFPWQVLLLGQTTAAAGALIHDNWVLTAAHAVYEKRMAASSLNIRMGILKRLSPH
YTQAWPEEIFIHEGYTHGAGFDNDIALIKLKNKVTINGSIMPVCLPRKEAASLMRTDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mRLLIFLGLLWSLVATLLGSKWPEPVFGRLVSPGFPEKYADHQDRSWTLTAPPGYRLRLYFTHFDLELSYRCEYDFVKLSSGTKVLATLCGQESTDTEQAPGRDTFYSLGPSLKVTFHSDYSNEKPFTGFEAFYAAEDVDECRVSLGDSVPCDHYCHNYL
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2"
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/tissue_type="Liver, normal. 5 mc/clone_lib="NCI_CGAP_Li9"
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/db_xref="taxon:10090"
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/db_xref="GI:15530225"
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                                                                                                                              ProGlyGluTyrAlaAsnAspGlnGluArgArgTrpThrLeuThrAlaProProGlyTyr 40
                                        Arg 41
                                                                                        Similarity:
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers abbreviations are used to associate primary accession numbers in the feature table with their source databases: Em:, EMBL; Sw:, SMISSPROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORNPEP database can be found at
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AL591032
AL591032.19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP22-211A10 from the RPCI-22 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-MAR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   corresponding to the overlapping clone, as we submit sequences with
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be approximately 160bp by restriction digest data."
a 50972 c 49570 g 51844 t
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/chromosome="4"
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Sequencing vector: M13: M77815; 0% of reads
Sequencing vector: plasmid; L08752; 99% of reads
Chemistry: Dye-terminator; 6% of reads
Chemistry: Dye-terminator Big Dye; 93% of reads
Consensus quality: 224154 bases at least Q40
Consensus quality: 224173 bases at least Q20
Consensus quality: 224186 bases at least Q20
Insert size: 22412; sum-of-contigs
Insert size: 22415; 2.4% error; agarose-fp
Quality coverage: 20.42x in Q20 bases; sum-of-contigs
Coverage: 21.08x in Q20 bases; agarose-fp
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Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL606969 224312 bp DNA 1:
Mus musculus chromosome 4 clone RP23-331P21,
PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 numquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 15, 2002 this sequence version replaced g1:22204261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 224312)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: bM331P21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ramsay,H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                       1 178012: contig of 178012 bp in length
178013 178112: gap of 100 bp
178113 224312: contig of 46200 bp in length.
Location/Qualifiers
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                                                                                                                                                                                                                      /note="assembly_fragment:07594
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178113. .224312
                                                                                                                                                              /note="assembly_fragment:01204
fragment_chain:1"
55510 c 55759 g 57660 t
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1. .178012
                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-MAY-2000) Wallis R., Department of Biochemistry, Glycobiology Institute, University of Oxford, South Parks Road, Oxford OX1 3QU, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interaction of mannose-binding protein with associated serine proteases: effects of naturally occurring mutations J. Biol. Chem. 275 (40), 30962-30969 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus partial mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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37. .2034
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Percent Similarity:
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Search completed: January 11, 2003, 12:10:20 Job time: 3228 secs
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                                  145 CGC 147
                                                                   41 Arg 41
                                                                                                    /product="mannose-binding protein associated serine protease-2" 516\ a 544\ c 507\ g 470\ t .
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen •

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Perfect score:
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-Q-Cgn2_1/USPT0_Spool/US0874199/runat_10012003_092045_2707/app_query.fasta_1.199
-DB-Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPELT-0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cd1 -LIST=60 -DCCALIGN=200 -THR_SCORE=pct -THK_MAX=100
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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and is derived
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  100.0
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238
1 TPLGPKWPEPVFGRLASPGF
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US-09-874-238-3
US-09-764-853-143
US-09-833-381-1924
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## ALIGNMENTS

US-09-874-198-3

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Sequence 3, Application US/09874198

Fatent No. US20020082208A1

GENERAL INFORMATION:

APPLICANT: Jensenius, Jens Chr.

APPLICANT: Thiel, Steffen

TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING EN:

Sequence 3, Appli
Sequence 3, Appli
Sequence 143, App
Sequence 143, App
Sequence 1924, Ap

FRICA APPLICATION NUMBER: US/09/874,198
Sequence 1924, Ap

FRICA APPLICATION NUMBER: 09/054,218
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PRIOR APPLICATION NUMBER: 60/042,678 PRIOR FILING DATE: 1997-04-03 NUMBER OF SEQ ID NOS: 8

FILING DATE: 1998-04-02

SOFTWARE: FastSEQ for Windows Version

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US-09-874-198-1 (1-41) x US-09-874-238-3 (1-2475)
                                                                                                                               Alignment Scores:
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Patent No. US20020082209A1
GENERAL INFORMATION
                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2475
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                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND TITLE OF INVENTION: USES FOR IT FILE REFERENCE: 09011-002003

CURRENT APPLICATION NUMBER: US/09/874,238

CHRENT FILING DATE: 2001-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jensenius, Jens Chr. APPLICANT: Thiel, Steffen
                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-04-03 NUMBER OF SEQ ID NOS: 8
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TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LOCATION: (37)
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LOCATION: (37)...(2094)
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OR FILING DATE: 1998-04-02
OR APPLICATION NUMBER: 60/042,678
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Best Local Similarity:
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US-09-764-853-143/c
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                                                          SOFTWARE: Fast
SEQ ID NO 1924
LENGTH: 742
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APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06
                                                                                                                                                                                                                                              Sequence 1924, Application Patent No. US20020132090A1 GENERAL INFORMATION:
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SEQ ID NO 143
LENGTH: 810
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                                                                                                                        APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR APPLICATION NUMBER: 0000-02-29
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CURRENT FILING DATE: 2001-01-17
                                                                                            NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
NAME/KEY: misc_feature
               FEATURE:
                              ORGANISM: Homo sapiens
                                                TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                606 CCCWTCTGGGATTCAAAGGAGCCCGTMTGCATCGCTGCTTGCGGCGGAGTGATCCGCAAT 547
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PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LEGTH: 1988
TYPE: NO.
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Query Match:
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; OTHER INFORMATION: n = A,T,C
US-09-833-381-1924
RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SHIMKETS, RICHARD A
APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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No.:
                                 1504 TGTCACTGGCTGCTTGAGGCTCCTGAGGGCCAGCGG 1539
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CATION: (178)..(1752)
004-551-21
                                                                                                    1444 GGCACCACCGGCCGCATCGTCTCCCAGGCTTCCCGGGCAACTACAGCAACAACCTCACC :1503
                                                                                                                                                                         1384 CCCTTCTGGGATTCAAAGGAGCCCGTCTGCATCGCTGCTTGCGGGGGGAGTGATCCGCAAT 1443
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                                                                                                                          12 -----PheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGlu 29
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                                                             30 ArgArgTrpThrLeuThrAlaProProGlyTyrArg 41
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (178)...(1752)
; OTHER INFORMATION: n 20
US-10-004-551-19
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; LOCATION: (178)...(1752)
; OTHER INFORMATION: n 2077 can be
us-10-004-551-17
             Alignment Scores:
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APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
                                                                                                                                          LENGTH: 2127
TYPE: DNA
ORGANISM: Homo s
                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/004,551
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
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APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: 15966-559
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PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
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CURRENT FILING DATE: 2001-12-05
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TYPE: DNA
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US-10-004-551-13
Sequence 13, Application US/10004551
Publication No. US20030004310A1
GENERAL INFORMATION:
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Query Match:
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NUMBER OF SEQ ID NOS: 110
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 23
LENGTH: 2143
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
APPLICANT: SHIMKETS, RICHARD A
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APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
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LOCATION: (178).
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Percent Similarity:
Best Local Similarity:
Query Match:
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; LOCATION: (178)..(3159);

; OTHER INFORMATION: n 1755

US-10-004-551-15
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Query Match:
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US-10-004-551-13
                                                                                                Alignment Scores:
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SEQ ID NO 15
LENGTH: 3879
TYPE: DNA
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LENGTH: 3863
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
CURRENT APPLICATION NUMBER: US/10/004,551
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
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US-09-917-800A-1712
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OR FILING DATE: 2001-07-09
BER OF SEQ ID NOS: 1740
SEQ ID NO 1712
SEQ ID NO 1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
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PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
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nt No. US20020119462A1
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13 -----GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArg 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 ArgArgTrpThrLeuThrAlaProProGlyTyrArg 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 -----PheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGlu 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL INFORMATION:
                                                                                          4 GlyProLysTrpProGluProValPhe-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/298,884 FILING DATE: 2001-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/295,798 FILING DATE: 2001-06-06 APPLICATION NUMBER: US 60/297,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/290,645 FILING DATE: 2001-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/292,336
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Castle, Arthur
Elashoff, Michael
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41.18%
31.37%
35.08%
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Matches:
Conservative:
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Indels:
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: LENGTH: 1480
: TYPE: DNA
: ORGANISM: Homo s
US-09-919-497-39
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Best Local Similarity:
Query Match:
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US-09-925-302-168
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    Alignment Scores: Pred. No.:
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US-09-919-497-39
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SEQ ID NO 168
LENGTH: 1148
                                                                                                                                        SOFTWARE: PatentIn version 3.0 SEQ ID NO 39
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TITLE OF INVENTION: Nucleic Acids, Proteins and FILE REPERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270
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                                                                                                                                                                         PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/919,497 CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/221,735 PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER FILE REFERENCE: B0801/7225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
                                                                                                                                                                                                                                                                                                                   APPLICANT: Mutter, George L.
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ORGANISM: Homo sapiens
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                                  US-09-808-602-92
                                                   RESULT 15
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LENGTH: 1480
TYPE: DNA
Sequence 92, Application US/09808602 Patent No. US20020155115A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-WO CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 3950
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Local Similarity:
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                                                                                                      ThrAlaProProGly 39
                                                                                                                                                                             LeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArgArgTrpThrLeu 34
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Scherf, Uwe
Gene Logic, Inc.
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Alignment Scores: Pred. No.:
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                                                                                                                                             SEQ ID NO 2256
LENGTH: 2493
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2256, Application US/09880107 Patent No. US20020142981A1
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                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILLING DATE: 2001-06-14 PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14 PRIOR APPLICATION NUMBER: US 60/237,054 PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 3950
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CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
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TYPE: DNA
ORGANISM: Hom
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TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding
FILE REFERENCE: 15966-697 CIP
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Gene Expression Profiles FILE REFERENCE: 44921-5028-WO
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                                                                                      FEATURE:
OTHER INFORMATION:
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Shimkets, Richard
Herrman, John L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mishra, Vishnu
Mezes, Peter S
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Indels:
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Conservative:
                                                                                        No.
                                                                                        US20020142981A1 M14058
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1003386CB1
US-10-044-090-613
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Best Local Similarity:
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DB:
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Best Local Similarity:
                           GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION /
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511,006/37-21(1029)50
FILE REFERENCE: 16511,006/37-21(1029)50
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 3224
LENGTH: 354
TYPES. NAS
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CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 613
LENGTH: 2555
                                                                                                                                                                                                                                                                              Sequence 3224, Application US/09960352
Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLICANT: Olga Bandman
FITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Bos taurus
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Gaps:
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US-09-960-352-10119

Sequence 10119, Application US/09960352

Patent no. US20020137139A1

GENERAL INFORMATION:
APPLICANT: Harren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C
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Best Local Similarity:
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Best Local Similarity:
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SEQ ID NO 8661
LENGTH: 392
TYPE: DNA
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Wathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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OTHER INFORMATION: Clone ID:
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US-08-991-408-1
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                                                                                              US-0,9-874-198-1 (1-41) x US-08-991-408-1 (1-5145)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/034
FILING DATE: 02-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,03
                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                            CORMATION FOR SEQ ID NO: EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Com
OPERATING SYSTEM:
                                                                13 GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArgArgTrp 32
                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 610-407-0701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: AT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/991,408
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-432-473-1
Search completed: January 11, Job time : 83 secs
                                                                                                                                                                                                                                             US-09-874-198-1 (1-41) x US-09-432-473-1 (1-5145)
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                                                                                                                                                                                                                                                                                                                                                                        Score:
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SEQ ID NO 1
LENGTH: 5145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/432,473 CURRENT FILING DATE: 1999-11-01 EARLIER APPLICATION NUMBER: 08/991,408 EARLIER FILING DATE: 1997-12-16 EARLIER APPLICATION NUMBER: 60/034,471 EARLIER FILING DATE: 1997-01-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ARLETH, ANTHONY J.
APPLICANT: WILLETTE, ROBERT N.
APPLICANT: ELSHOURBAGY, NABIL A.
APPLICANT: LI, XIAOTONG
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN
FILE REFERENCE: ATG-50038-D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
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                                                                                 2658 GAAATCAGCGCCACTCCTGGCCACCGA 2684
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                                                                                                                   33 ThrLeuThrAlaProProGlyTyrArg 41
                                                                                                                                                                                                    GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArgArgTrp 32
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Matches:
Conservative:
Mismatches:
Indels:
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US-08-866-650-4

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                 Alignment Scores:
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   Pred. No.:
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Best Local Similarity:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                            TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/866
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BETSON, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 9
                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 3919 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
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                                                                                NAME/KEY:
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                                                                  OTHER INFORMATION:
                                                                                                                                  ORGANISM:
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CLASSIFICATION:
                                                                                                                                                                                  TOPOLOGY:
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                                                               "human mTll protein"
Length:
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                      ; LOCATION: 648..368; OTHER INFORMATION: US-09-240-473-4
US-09-874-198-1 (1-41) x US-09-240-473-4 (1-3919)
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US-09-240-473-4
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Query Match:
                                                                                                             Pred. No.:
                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                          TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   NAME: Berson, Bennett J
REGISTATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 96:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
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TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
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                                                                                                                                                                                                   NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
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STREET: 1 South Pinckney Street
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                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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Matches:
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Indels:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA

TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:

PROTEIN

HUMAN CARDIAC/BRAIN TOLLOID-LIKE

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GENERAL INFORMATION:
APPLICANT: ARLETH, ANTHONY J.
APPLICANT: ALLETTE, ROBERT N.
APPLICANT: ELSHOURBAGY, NABIL A.
APPLICANT: LI, XIAOTONG
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN
FILE REFERENCE: ATG-50038-D1
CURRENT APPLICATION NUMBER: US/09/432,473
CURRENT FILING DATE: 1999-11-01
EARLIER APPLICATION NUMBER: 08/991,408
EARLIER APPLICATION NUMBER: 60/034,471
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APPLICATION NUMBER: 60/034,47:

EILING DATE: 02-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: ATG-
TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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OPERATING SYSTEM: DOS
SOFTWARE
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CITY: VALLEY FORGE
STATE: PA
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1997-01-02 NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3690
TYPE: DNA
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                     TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 370
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1203 GAAATCAGCGCCACTCCTGGCCACCGA 1229
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                                                   FEATURE:
                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                     TYPE: n
                 NAME/KEY:
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                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 53703
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 OTHER INFORMATION:
                                                                   ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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                                                                                                                       TOPOLOGY:
                                                                                                                                                   nucleic acid
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                                                                                                                                                                   3919 base pairs
                 CDS
648
                                                                                                                   linear
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                                                                 Homo sapiens
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/product= "human mTll protein"
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Conservative:
Mismatches:
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US-08-872-757-3
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Best Local Similarity:
Query Match:
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US-08-377-292-1
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Sequence 3, Application US/08872757 Patent No. 6258584 GENERAL INFORMATION:
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Patent No. 5693615
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                                                                                                                                                                   1827
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,292
                                                                                                 1887 CAGCTGGTGGCCCCCCCCCGGTACCGC 1913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2487 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                   No . .
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FILING DATE:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                33 ThrLeuThrAlaProProGlyTyrArg 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 45239-8707
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Matches:
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                                                                                                               US-08-991-408-3
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Query Match:
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                                                           Sequence 3, Application US/08991408 Patent No. 6008017 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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             APPLICANT:
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TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
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APPLICATION NUMBER: US/08
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
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APPLICANT:
APPLICANT:
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APPLICANT:
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CTTY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                 No . .
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           WILLETTE, ROBERT N. ELSHOURBAGY, NABIL A.
                                            ARLETH, ANTHONY J.
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US-09-874-198-1 (1-41) x US-08-872-757-3 (1-3546)
2326 GCCATCTCCAGCACCCCGGGCACCGG 2352
                                                                             2266 GGTACCATCACCAGCCCCAACTGGCCTGACAAGTATCCCAGCAAGAAGGAGTGCACCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                   ThrLeuThrAlaProProGlyTyrArg 41
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1155 Avenue of the Americas
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RECOMBINANT C-PROTEINASE AND
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Indels:
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                          Percent Similarity:
Best Local Similarity:
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US-08-611-729A-7
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US-08-611-729A-7/c
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          Query; Match:
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                                                            Score:
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APPLICANT: Henriq
                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICATION NUMBER: US,
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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REFERENCE/DOCKET NUMBER: 73
ELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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STATE: New Yor
                                                                                                                                                                                                     LENGTH: 4483 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Gray, Grace E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myat, Anna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lewis,
                                                                                                                                CDS
332..4102
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                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                              (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAR-1996
                                                                                                                                                                         DNA (genomic)
            44.7
70.00
53.85%
46.15%
29.41%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE AND PROTEIN SEQUENCES OF THE SERRATE GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/611,729A
                                                                                                                                                                                                                                                                                                                                          7326-037
                                                       Length: Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                          Mismatches:
             Indels:
                                           Conservative:
2673
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                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-872-757-1
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                                                       US-09-874-198-1 (1-41) x US-08-872-757-1 (1-2457)
                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                     Score:
                                                                                                                                                                                                                                          US-08-872-757-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1605 GGCCCC---GCGTCTGACCCGCAGCCATCGATCACTCTGCAGGCCCCGGCCAGGGCAC 1552
                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 415-854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sieron, Aleksander
TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
TITLE OF INVENTION: PROCESSES; METHODS AND USES
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                      No . .
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 415-854-36
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
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13 GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArgArgTrp 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 10-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                       2457 base pairs
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                                                                                                                                                                                                                                                                                                                                   unknown
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10-JUN-1997
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69.00
58.62%
44.83%
28.99%
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                                                                                                                                              Length:
Matches:
Conservative:
                                                                                                            Mismatches:
Indels:
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CURRENT APPLICATION DATA:

CLASSIFICATION: FILING DATE: APPLICATION NUMBER:

23-APR-1997 N: 435

us/08/839,008

OPERATING SYSTEM: SOFTWARE: Patent:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS PatentIn Release #1.0, Version #1.25

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Query Match:
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                                                                                                                                                          SEQ ID NO 4
LENGTH: 3955
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                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09214278 Patent No. 6291210
                                                                                                                                                                                                                                                          APPLICANT: Sakano, Seiji
APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/214,278
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
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APPLICATION NUMBER: 08/563,697
FILING DATE: 28 NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50384
                                                                                                                                                                                             SOFTWARE:
                                                                                                                                          LENGTH: 39
TYPE: DNA
                                  LOCATION: (12)..(3725)
NAME/KEY: sig_peptide
LOCATION: (12)..(89)
NAME/KEY: mat_peptide
LOCATION: (90)..(3725)
                                                                                                                      ORGANISM: Homo sapiens
                                                                                         NAME/KEY:
                                                                                                         FEATURE
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MOLECULE TYPE:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 GTGGCAAGTGAGGGTTTTCCCCCAACCTCTACCCCCCAAACAAGAAGTGCATCTGGACAATT 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                         242 ACGGTGCCCGAGGGG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 CCCAACTACACGAGACCTGTGTTCCTGTGCGGAGGGGACGTGACCGGGGAGTCAGGTTAC 181
                                                                                                                                                                                                                                                                                                                                                                                          214-278-4/c
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31.09%
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Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                      Score:
                                                                                                  Pred. No.:
                                                                                                                                        Alignment Scores:
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   Best Local Similarity:
                               Percent Similarity:
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ZIP: 10036-2711
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
COMPATIBLE CONTROLLER
COMPATIBLE CONTROLLER
COMPATIBLE CONTROLLER
CON
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APPLICANT: Ish-Ho
APPLICANT: Henriq
                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPA
OPERATING SYSTEM: PC-DO
SOFTWARE: PatentIn Rela
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 732
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1840 CCATGGGGGCCACACACGCCGGAG-------GCTGCTGCTGTGCCAGGCATCCCA 1796
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                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/400,159 FILING DATE: 07-MAR-1995
                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4464 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66141 PENNIE
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Gray, Grace E.
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                                                                                                                                                                                                                                                                              unknown
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Fleming, Robert J.
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Matches:
   Conservative: Mismatches:
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R FILING DATE: 1997-08-18
R APPLICATION NUMBER: 60/09
R FILING DATE: 1997-08-18
R FILING DATE: 1997-08-18
R FILING DATE: 1997-08-18

60/056,360 8-18 60/055,684 APPLICATION NUMBER: 60/055,964

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Percent Similarity:
Best Local Similarity:
Query Match:
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; LOCATION: (642)
; OTHER INFORMATION: n
US-09-227-357-37
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EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08839008 Patent No. 5916758 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
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                                                                              APPLICANT: Hurle, Mark R
APPLICANT: McDonnell, Peter C
APPLICANT: McNoulty, Dean E
APPLICANT: Rosen, Craig A
APPLICANT: Siemens, Ivo R
APPLICANT: Young, Peter R
APPLICANT: Young, Peter R
APPLICANT: Yue, Tian-Li
TITLE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor
NUMBER OF SEQUENCES:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
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STREET: 709 Swedeland MCITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
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Matches:
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Query Match:
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                                                                                                                                                                                                                                                        Patent No. 5916758
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     Sequence 6,
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NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P503
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-70-5096
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
 COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline
STREET: 709 Swedeland
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APPLICATION NUMBER: 08/5
FILING DATE: 28-NOV-1995
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                                                              STREET: 709 Swederanu CITY: King of Prussia
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                                                           STATE:
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Youe, Tian-Li
Smoot
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McNulty, Dean E
Rosen, Craig A
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                  Alignment Scores:
                                                                                                                US-08-839-008-1
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: APPLICANT:
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1537 base pairs
                                                                                                                                                                                                                                                                                   RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/563,697
APPLICATION NUMBER: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Smooth Muscle Cell-Derived NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                     No.:
                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                           TOPOLOGY:
                                                                                                                                                        STRANDEDNESS:
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McNulty, Dean E
Rosen, Craig A
Siemens, Ivo R
Young, Peter R
Young, Tian-Li
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709 Swedeland
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                                                                                                                                                                                                                                                                       P50384
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Matches:
           Mismatches:
Indels:
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Conservative:
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                                                                    length:
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RESULT 5
US-09-227-357-37/c
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                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/051,920 EARLIER FILING DATE: 1997-07-08 EARLIER APPLICATION NUMBER: 60/052,733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: 123 FILE REFERENCE: PZ010P1
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                                                                                               APPLICATION NUMBER: 60/0
PTEITING DATE: 1997-08-18
                                                                                                                                                                  APPLICATION NUMBER: 60/0
FILING DATE: 1997-08-18
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APPLICATION NUMBER: 60/051,928
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/
FILING DATE: 1997-08-18
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FILING DATE: 1997-08-18
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FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/051,931
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                                                                                   APPLICATION NUMBER:
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FILING DATE: 1997-08-18
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                                FILING DATE:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4360 hasa
                                                                                                                                                                                                                                                                                                                 Patent No. 5916758
                                                                                                                                                                                                                                                                                                                                 Sequence 8,
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: Hurle,
                                                                                                        APPLICANT: Young, Peter R
APPLICANT: Yue, Tian-Li
TITLE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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HYPOTHETICAL: NO
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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LOCATION:
                                  COUNTRY: U. ZIP: 19406
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                                                                STATE: PA
                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                               31 ArgTrpThrLeuThrAlaProProGlyTyrArg 41
                                                                              CITY: King of Prussia
                                                                                                 ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
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Yue, Tian-Li
smooth
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McNulty, Dean E
Rosen, Craig A
Siemens, Ivo R
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Percent Similarity:
Best Local Similarity:
Query Match:
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; ORGANISM: Homo sapiens US-09-381-779-1
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US-09-381-779-1
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                                                     SEQ ID NO 1
LENGTH: 2492
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                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                    APPLICANT: Simpson, John W.

TITLE OF INVENTION: METHOD FOR IDENTIFYING A NUCLEIC ACID SEQUENCE
FILE REFERENCE: Cura-8 US 15966-508
CURRENT APPLICATION NUMBER: US/09/381,779
CURRENT FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US.S.N. 60/054,887
PRIOR APPLICATION NUMBER: US.S.N. 60/054,887
PRIOR APPLICATION NUMBER: PCT/US98/16548
PRIOR APPLICATION NUMBER: PCT/US98/16548
PRIOR APPLICATION NUMBER: PCT/US98/16548
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SEQUENCE CHARACTERISTICS:
                                                                                         SOFTWARE:
                                                                                                              NUMBER OF SEQ ID NOS:
                                      TYPE: DNA
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            262 ACGGTCCCCGAGGC 276
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                                                                                         PatentIn Ver. 2.0
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SYSTEM: PC-DOS/MS-DOS
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Alignment Scores:

5.1.3

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Command line parameters:

-MODEL-frame+_D2n.model -DEV-xlp
-O_cgn2_1/USBTO_Spool_US09874198/runat_10012003_092044_2595/app_query.fasta_1.199
-OB-Issued_Patents_NA -OFMT-fastap -SUFFIX=P2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=60 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20
-MODE=LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-MSER=US09874198_@cGN_1_1_31_@runat_10012003_092044_2595 -NCPU=6 -ICPU=3
-NO_XLDXY -NO_MMAP -LARGDUERY -NG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-839-008-6
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RESULT 1
US-08-470-350B-1
; Sequence 1, Application US/08470350B
; Patent No. 5684126
                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Li, Xiao
APPLICANT: Snyder, Sc
TITLE OF INVENTION: E
TITLE OF INVENTION: E
NUMBER OF SEQUENCES:
                              ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Command line parameters:
-MODEL-frame+_p2n.model -DEV-xlp
-MODEL-frame+_p2n.model -DEV-xlp
-Q-/cgn2_1/USPTQ_spoo1/US09874198/runat_10012003_092044_2571/app_query.fasta_1.199
-DB-EST -QFMT-fastap -SUFFIX-p2n.rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT=0
-UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-60
-DCCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN-20 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MIXLEN-200000000
-USER-US09874198_@CGN_1_1_1716_@runat_10012003_092044_2571 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEC_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS-1 -XGAPOP-10 -XGAPEXT=0.5 -FGAPOP-6 -FGAPEXT=7
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Listing first 60 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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BQ654231 911 bp mRNA linear EST 15-JUL-2002 AGENCOURT_8493289 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6299026
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Tissue Procurement: CGAP (Stanford)
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lib="NHH_MGC_100"
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/lab_bost="0H10B (phage resistant)"
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRIXXhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
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/db_xref="taxon:9606"
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AGENCOURT_8299192 NIH_MGC_100 Homo 5', mRNA sequence.
BQ648641
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High quality sequence start: 5
High quality sequence stop: 461.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Tissue Procurement: CGAP (Stanford)
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="hH10B (phage-resistant)"
/note="Organ: liver; Vector: psissip: Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
ILRT (Life Technologies). Note: this is a NIH_MGC
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Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/tlab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 939)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                    5', mRNA sequence
BQ644570
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AGENCOURT_8490607 NIH_MGC_100
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Plate: LLCM2479 row: e column:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Tissue Procurement: CGAP (Stanford)
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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1 (bases 1 to 921)
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//db_xref="taxon:9606"
//clone="IMAGE:6283375"
//clone=lib="NIH_MGC_100"
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//lab_host="PH10B (phage_resistant)"
//note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb Libzary constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 975)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CGAP (Stanford)
                                                                                                                                                                                                                                                                              975 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8488545 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6296149
5', mRNA sequence.
BQ646367
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Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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GCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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5', mRNA sequence:
BQ653181
                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
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National Institutes of Health, Mammalian
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cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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                                                                                                                                                                   Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 238)

1 (bases 1 to 238)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martlh,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA896425 238 bp mRNA linear EST 06-APR-: vy31e05.rl Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:1297088 5' similar to TR:000187 000187 MASP-2 PROTEIN. ;,
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washb-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
AA896425
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                                                                                                                                                 The WashU-HHMI Mouse EST Project
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/lab_host="hH10B (phage resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: xhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCACCAAc(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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/db_xref="taxon:9606"
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                        Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Iakimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
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BB870802
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BB870802
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Location/Qualifiers
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Unpublished (2001)
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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RIKEN full-length enriched, pooled tissues, intestinal
etc. Mus musculus cDNA clone G630025E18 5', mRNA sequen
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/strain="C57BL/6 x CBA"
/db_xref="taxon:10090"
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/clone_lib="Stratagene mouse
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          67
Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-171 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
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axillary lymph node, dev_stage=adult, sex=male),
(tissue_type=jejunal and colic lymph node, dev_stage=adult,
sex=male), (tissue_type=gall bladder, dev_stage=adult,
sex=male), (tissue_type=gall bladder, dev_stage=adult,
sex=male), (tissue_type=spinal cord, dev_stage=11 days
embryo), (tissue_type=brain, dev_stage=13 days embryo),
(tissue_type=brain, dev_stage=13 days embryo),
(tissue_type=lung, dev_stage=13 days embryo),
(tissue_type=lung, dev_stage=13 days embryo),
(tissue_type=brain, dev_stage=14 days embryo),
(tissue_type=brain, dev_stage=10 days pregnant
adult, sex=female), (tissue_type=cortex, dev_stage=10 days
neonate), (tissue_type=cortex)

(tissue_type=lung, dev_stage=10 days
neonate), (tissue_type=cortex)

(tissue_type=female), (tissue_type=femal
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dev_stage=16 days neonate, sex=male),
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intestinal mucosa, etc."
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/db_xref="taxon:10090"
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (I
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagaw
Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
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BB871372 RIKEN full-length enriched, adult male ç
musculus cDNA clone G630029B14 5', mRNA sequence
BB871372
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                          further details.
e mouse tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Konno, H., Fukunishi, Y., Shibata, K.,
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                              /tissue_type="gall bladder"
/dev_stage="adult"
                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="G630029B14"
                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                    /sex="male"
                                                                                                                                                             /clone_lib="RIKEN full-length
tissues ; (tissue_type=cerebellum
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d, adult male gall
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ma, Kanagawa 230-0045, Japan
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 416)
1 (bases 1 to 416)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                            Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor - human ;, mRNA sequence.
W14100
W14100.1 GI:1288286
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416 bp mRNA linear EST 10mb27h04.rl Soares mouse p3NMr19.5 Mus musculus cDNA clone IMAGE:330679 5' similar to PIR:JN0883 JN0883 Ra-reactive
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The WashU-HHMI Mouse EST Project
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sex=male), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed)
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(tissue_type=cerebellum, dev_stage=0 day neonate,
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:330679"
                                                                                                                                                             Location/Qualifiers
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AA237253
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                                                                                                                                                                                             Contact: Marra M/Mouse EST Project Washington University School of MedicineP 4444 Forest Parkway, Box 8501, St. Ld Tel: 314 286 1800

Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubigeisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                Possible reversed clone: similarity on wrong Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 439.
Location/Qualifiers
                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                        Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 546)
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                                                                                                                                                                              mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Mayne State University)."
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/db_xref="taxon:10090"
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/clone="IMAGE:680532" /clone\_lib="Soares mouse NML"

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ACCESSION
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                          MGI:419936

Possible reversed clone: similarity on was Seq primer: -28ml3 rev2 ET from Amersham
                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                               WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton Parkway, Box 8501, St. La
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA238260 552 bp mx15a01.rl Soares mouse NML Mus similar to SW:CRAR_HUMAN P48740 RA-REACTIVE FACTOR PRECURSOR ;,
                                                                                                                                                                                                                   Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                   Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 552)
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              quality sequence stop: 423.
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The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI529228 586 bp mRNA linear EST 18-MAR-1999 ui61d09.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1886897 5' similar to TR:000187 000187 MASP-2 PROTEIN.;,
                                                                                                                          Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                  IMAGE Consortium (info@image.llnl.gov)
MGI:971221
                                                                                          Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 586)
                                                    This clone is available royalty-free through LLNL;
                                                                     Email: mouseest@watson.wustl.edu
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Possible reversed clone: similarity
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/tissue_type="Liver"
/lab_host="DH10B"
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Email: cgapbs-r@mail.nih.gov.
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 600)
                                                                                                                                                                                                                                                                                                                  mRNA sequence.
BF532409
                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                 EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTTGCG and 3' end primer CGACCTGCAGCTGAGACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACCTGTGG, 3' site CACCTGTGG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library
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(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
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/db_xref="taxon:10090"
/clone="IMAGE:1886897"
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/sex="female"
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Sciurognathi; Muridae
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                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Januel: 81-45-503-9222
Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                              Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishi,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus
BB653589
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                             Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone_lib="NCI_CCAP_Li9"
/clone_lib="NCI_CCAP_Li9"
/clone_lib="NCI_CCAP_Li9"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 175 c 156 g 144 t
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US-09-874-198-1 (1-41) x BB653589 (1-699)
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ProGlyGluTyrAlaAsnAspGlnGluArgArgTrpThrLeuThrAlaProProGlyTyr 40
                                                                                                       ACACTTCTGGGTTCAAAGTGGCCTGAACCTGTATTCGGGCGCCCTGGTGTCCCCTGGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was cleaved with BamHI and XhoI. Vector: a modified pBlueScript KS(+) after bulk excision from Lambda FLC I. Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology Elm and Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully acknowledge."
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Project of Genome Exploration Research Group in Rik
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/db_xref="taxon:10090"
/clone="C730007H22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI226038 729 bp mRNA linear EST 29-OCT-
uj08e08.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1891334 5' similar to TR:000187 000187 MASP-2 PROTEIN. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 729)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:975658
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                                                                                                                                                                                   151
                                                                                                                                                                                                                                 sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
3 221 c 187 g 167 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
                                                                                                                                                                                                                                                                                                                     [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18s-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG) XhoI show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Sugano mouse liver mlia"
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  1.37e-11
183.00
85.37%
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RESULT 18
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                                                     CGC 249
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CCAGAGNAGTATGCTGACCATCAAGATCGATCCTGGACACTGACTGCACCCCCTGGCTAC
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 752)
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602024289F1 NCI_CGAP_Li9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
Plate: LLAN9437 row: b column: 24
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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BF233497
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 218 c 186 g 168 t
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/db_xref="taxon:10090"
/clone="IMAGE:4159415"
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RESULT 20
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                                                                                                           Arg 41
                                                                                                                                             Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11143 row: a column: 23
High quality sequence stop: 767.
BF236712 884
602028006F1 NCI_CGAP_Li9 Mus
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:5052574"
/clone_lib="NCI_CAP_Li9"
/clone_lib="NCI_CAP_Li9"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 247 c 221 g 189 t
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/db_xref="taxon:10090"
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Mismatches:
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\GE:4163448 5',
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                                                                                                                                                                                                           41 Arg 41
                                                                                                                                        92
                                                                                                                                                           21 ProGlyGluTyrAlaAsnAspGlnGluArgArgTrpThrLeuThrAlaProProGlyTyr 40
                                                                                                                                        Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9447 row: k.column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 884) 1 (bases 1 to 884) NIH-MGC http://mgc.nci.nih.gov/...
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BF236712
BF236712.1 GI:11150598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Strain="FVB/N"
/Strain="FVB/N"
/Strain="FVB/N"
/Clone="INAGE:4163448"
/Clone=1b="NGI_CGAP_Li9"
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/Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 256 c 252 g 185 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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183.00
85.37%
78.05%
76.89%
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                     Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                  0 0 6 3 2 4
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-MODEL-frame+_p2n.model -DEV=xlp
-Q=/cg12_1/USPTO_spool/US09874198/runat_10012003_092043_2552/app_query.fasta_1.199
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-DB=N_Genceseq_10102 -OFMT-fastap -SUFFIX=p2n.rng -MINNATCH=0.1 -LOOPCL=0
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=7
-YGAPPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Ygapop 6.0 , Fgapext
Fgapop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  January 11, 2003, 11:06:19; Search time 351 Seconds (without alignments) 263.054 Million cell updates/sec
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
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                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqn-embl/WA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/WA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/WA1991.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/WA1992.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/WA1994.DAT:*
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/SIDS2/gcgdata/geneseq-geneseqn-embl/WA1997.DAT:*
/SIDS2/gcgdata/geneseq-geneseqn-embl/WA1997.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
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7.0
7.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

6555555555555444444444444444444444	000	Result No.
88 9999999 2211111		. score
33333333333333333333333333333333333333	100.0 100.0 39.3 39.3 39.3 39.1 39.1	Query Match
13895 21127	2472 3106 810 810 810 810 363 397	Length 1
10000000000000000000000000000000000000	22 22 23 21 21	DB
AAFF33985 AAF74442 AAF74443 AAF74443 AAF74443 AAF74443 AAF74433 AAF74433 AAF74433 AAF74433 AAF744363 AAF744363 AAF18149 AAK53509 AAK545097 ABK355698 AAF18149 AAK590113 AAK500113 AASS00114 AASS00113 AASS00113 AASS00113 AASS00114 AASS00113 AASS00113 AASS00113 AASS00114 AASS00114 AASS00113 AASS00113 AASS00114 AASS00113 AASS00114 AASS00113 AASS00114	AAD24224 AAS85321 ABA06477 AAS31599 ABK43587 AAC00227 AAH43512	ID
Human Seriti Human PRO11 Human PRO19 Human PRO19 Human PRO11 Human PRO11 Human PRO11 Human PRO11 Human PRO18 Human PRO18 Human SE26 Drosophila Rat sequenc Rat von Ebr Lung cances Gene #2196 Human endon Human compl Complement Gene #206 Human conpl Complement Gene #200 Human conpl Complement Gene #200 Human conpa Conpa Human cona Human cona	man man NA Man man	Descriptio
nucleo nucleo nucleo nucleo nucleo nucleo nucleo nucleo nucleo encodi nucleo nucleo nucleo encodi	ASP-2 coding n DNA SEC coding coding n oding coding coding n ecreted ecreted coding	ion

ALIGNMENTS

RESULT 1
AAD24224
ID AAD24224 standard; cDNA; 2472 BP.

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and spontaneous recurrent abortion. The pharmaceutical composit comprising MASP-2 inhibitor is useful for treating inflammatory % \left( 1\right) =\left( 1\right) +\left( 1\right) +\left(
                                                                                                         treating infections caused by microbes such as fungus, yeast, retrovirus (e.g. human immunodeficiency virus (HTV)), or pathogenic bacteria which are resistant to at least one antibiotic medicament or multiresistant. The polynucleotide encoding MASP-2 is useful for treating patients deficient in MASP-2. The invention also discloses MASP-2 assays which are useful for determination of MASP-2 activity or levels in patients suffering from e.g. infections, inflammatory disorded the state of the suffering from e.g. infections, inflammatory disorded the suffering from e.g. infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to use of a polypeptide derived from mannan-binding lectin (MBL) associated serine protease-2 (MASP-2) for producing a pharmaceutical composition. MASP-2 is a complement-fixing enzyme and involved in lectin pathway of complement activation The pharmaceutical composition comprising MASP-2 is useful for the pharmaceutical composition comprising manner compris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for producing pharmaceutical composition, to treat bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
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P-PSDB; AAE14564, AAE14568.
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01-JUN-2001; 2001DK-0000870
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(THIE/) THIEL S.
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ement fixation; infection; microbe; retrovirus; HIV; abortion;
immunodeficiency virus; pathogenic bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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82..2091
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37..81
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/transl_except= (pos:499..500, aa:His)
/transl_except= (pos:501, aa:Cys)
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decoding the alternative version of the
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                                                                pharmaceutical composition
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       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                      WPI; 2001-639362/73.
P-PSDB; ABG21134.
                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic (
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                                                                                                                                                                  biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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   31 - JAN - 2000;

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07 - JUN - 2000;

28 - JUN - 2000;

07 - JUL - 2000;

07 - JUL - 2000;
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO as for a company terms of the invention.
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                                                                                                                                                                                                                                                                                                                                             Human; gene therapy; neural disorder; immune system disorder; nuscular disorder; reproductive disorder; gastrointestinal dipulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation; ss.
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Match:
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 2000US-184664P.
2000US-186350P.
2000US-188974P.
2000US-190076P.
2000US-19123P.
2000US-20515P.
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2000US-211686P.
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   14-AUG-2000:
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2000US-225270P.
2000US-22547P.
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2000US-225758P.
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2000US-232399P.
2000US-232400P.
2000US-232401P.
2000US-23363P.
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Pred.

No . :

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DNAs. Thes muscular, renal and
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117 NOV 2000
01 DEC 2000
01 DEC 2000
05 DEC 2000
05 DEC 2000
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08 DEC 2000
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01-NOV 2000;
08-NOV 2000;
                                The present invention provides human cDNAs, proteins and related g DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular renal and proliferative disorders and inflammation. The present se
                                                                                     Claim 1;
                                                                                                           polypeptide is used condition -
                                                                                                                                                     WPI; 2001-476161/51.
P-PSDB; ABB10255.
  Sequence 810
                                                                                                                               Isolated nucleic acid molecule encoding an inflammation-associated
                                                                                                                                                                                    Rosen
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17-NOV-2000,
                        isa
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                        CDNA
                       , reproductive, of proliferative of the invention
                                                                                     SEQ ID
                                                                                                                                                                                    Barash
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2000US-251869P.
2000US-251989P.
2000US-251990P.
2000US-251990P.
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                                                                                     NO:
  181 A;
                        invention.
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                                                                                                                    in preventing, treating or
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                                                                                                                                                                                                         SCI INC
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   189 C;
                                                                                    859pp + Sequence Listing; English
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   249
  G;
187 T; 4 other;
                                                                proteins and related genomic
                                                                                                                  ameliorating a medical
                                           cardiovascular,
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Alignment Scores:

sequence

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AAS31599/c
ID AAS315
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            24-FEB-2000
02-MAR-2000
16-MAR-2000
17-MAR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
30-JUN-2000
07-JUL-2000
07-JUL-2000
11-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; calcium-binding protein; calcium flux; neurological disease; immune dysfunction; digestive disorder; neoplastic disease; blood disorder; infectious disease; gene therapy; immunosuppressive; antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200155304-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding novel human calcium-binding protein #23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486
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2000US-0189874.
2000US-0199076.
2000US-020515.
2000US-0204886.
2000US-0211335.
2000US-0211880.
2000US-0211880.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-02252964.
2000US-0225214.
2000US-0225266.
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93.50
46.15%
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Conservative:
Mismatches:
Indels:
Gaps:
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2000US-0229343

30-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000

08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

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Alignment Scores: Pred. No.:
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08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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01-DEC-
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                                                                                                                                                     The present invention relates to the isolation of novel human calcium—binding proteins (AAU19892-AAU19999), and cDNA and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amylotrophic lateral sclerosis, ALS), inmune dysfunction (e.g. severe combined immunodeficiency, SCID), indiseases (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). To novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit
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17-NOV-
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                                                                     proteins.

Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                     activities mediated by calcium-binding proteins. The polynucleotides the invention are also useful in gene therapy. AAS31577-AAS31654 represent cDNA sequences encoding for the novel human calcium-binding
                                                Sequence 810
                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecule encoding a calused in preventing, treating or ameliorating
                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB;
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2000US-0250160
2000US-0250391
2000US-0251030
2000US-025198
2000US-0251479
2000US-0251856
2000US-0251869
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Length:
Matches:
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2000US-0246474.
2000US-0246475.
2000US-0246476.
2000US-0246477.
2000US-0246477.
2000US-0246523.
2000US-0246525.
2000US-0246526.
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20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000;

2000US-0241787. 2000US-0241808. 2000US-0241809. 2000US-0241826. 2000US-0244617. 02-0CT-2000; 02-0CT-2000; 02-0CT-2000; 13-0CT-2000; 13-0CT-2000;

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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 07-JUN-2000
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14-JUL-2000
26-JUL-2000
26-JUL-2000
14-AUG-2000
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food addition farction; wound healing; cell proliferation; skin aging;
                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2001; 2001WO-US01332
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200155318-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel central nervous system protein #167.
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587/c
ABK43587 standard;
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 2000US-0180628.
2000US-0186340.
2000US-0189874.
2000US-0198123.
2000US-0198123.
2000US-0209467.
2000US-0209467.
2000US-0211135.
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22
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09 SEP 2000
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2000US-0234997

2000US-0234998

2000US-0235834

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2000US-02332080.
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2000US-0225447.
2000US-0225757.
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CC The invention describes an isolated nucleic acid molecule (1) encoding a CC novel central nervous system protein. (1) and polypeptides (III) encoded CC by (1), are used to treat a medical conditions and in diagnosis of a CC pathological condition. Disorders which are diagnosed or treated include autolumnume diseases e.g. rheumatold arthritis, hyperproliferative CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and CC amylotrophic lateral sclerosis, infections caused by bacteria, viruses CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, CC adenocarcinomas and tirritable bowel syndrome, reproductive system CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cardial cc respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cardial cc respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cardial cc respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cardial cc respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cardial cc respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cardial cc respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cardial cc respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cardial cc respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cardial cc respiratory disorders e.g. cardial continue of primary t.ssues, to regenerate tissues and in chemorlays cardial culture of primary t.ssues, to regenerate tissues and in chemorlays cardial c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 177; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2000;
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regenerate tissues and in chemotaxis.
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
        mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, denote there are also used in diagnostic, forensic,
                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo diagnostic, forensic, gene therapy and chromosome mapping procedu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides can also be used as a food additive or preservative to
                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted
gene therapy and chromosome mapping procedures.
                                                                                                                                                                                 The present sequence is one of a large number of 5' ESTs derived from
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                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET
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DB; AAG01729.
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                                                                                                                                                                                                                 1; SEQ ID 1733; 71pp + CD-ROM; English.
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                                                                                                                                                  g secreted proteins.
5' ESTs were not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
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RESULT 7
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             mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                              The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polya+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of
                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID 225; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                         diagnostic, forensic,
                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
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chromosome mapping; ss.
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Best Local Similarity:
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14-APR-2000;
20-APR-2000;
                 Claim
                                                                       New polypeptide for treating autoimmune disorders, compris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; protease; PRTS; gastrointestinal disorder; peptic esophagitis; indigestion; gastritie; cardiovascular disorder; reproductive disorder; hypertensive heart disease; myocardial infarction; autoimmune disorder; inflammatory disorder; rheumatoid arthritis; cell proliferative disorder; arteriosclerosis; cancer; epithelial disorder; eczema; endometriosis; neurological disorder; Huntington's disease; ss.
                                                   polynucleotides
                                                                                                                                                    WPI; 2001-611509/70
                                                                                                                                                                                                       Au-Young J, Bandman O, Lal
Tang YT, Burford N, Baughn
                                                                                                                                                                                                                                            Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W0200171004-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 397
                                                                                                                                P-PSDB;
                                                                                                                                                                                       Hafalia A,
                                                                                                                                                                                                                                                                                      (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                                     17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding protease PRTS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-DEC-2001
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                 <u>ن</u>
                                                                                                                              AAB47559
                                                                                                                                                                                                                                                                                    INCYTE GENOMICS INC
                                                                                                                                                                                                                                              Lu DAM,
               Page 122-23;
                                                                                                                                                                                                                                                                                                                      2000US-190708P.
2000US-193182P.
2000US-197086P.
2000US-199022P.
2000US-200227P.
                                                                                                                                                                                       Lu Y,
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                                                                                                                                                                                                                         Policky JL,
~Aman O, Lal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 86..2272
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                                                                                                                                                                                         Patterson
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             129pp; English
                                                                       comprises
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                                                                                                                                                                                     C;
                                                                     gastrointestinal, cardiovascular and ses novel human proteases (PRTS) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-397)
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                                                                                                                                                                                                       Nguyen DB,
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Conservative:
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Yao MG, Walia NK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mannan-binding lectin associated serine protease-3; MASP-3; MBL; human; mannan-binding lectin; complement; infection; cancer; cytostatic; immunomodulator; neuroprotective; anticonvulsive; antirheumatic; antiarthritic; antianemic; antiinflammatory; antipsoriatic; antidiabetic; antiatherosclerotic; ds.
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Novel pure mannan-binding lectin associated serine protease
                                                                 P-PSDB; AAB85060
                                                                                                                                                                                                                                                                                                    02-DEC-1999;
21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-2000; 2000WO-DK00659
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                                                                                             WPI; 2001-374820/39.
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                                                                                                                                                     Jensenius JC,
                                                                                                                                                                                                             (JENS/) JENSENIUS J C.
(THIE/) THIEL S.
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2000DK-0001126
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                                                                                                                                                        Thiel S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 91..2277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "MASP-3"
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Alignment Scores:

No.:

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and directly activates complement system through binding to MBL. The MASP-3 polypeptides, polynucleotides and modulators are useful for preparing a pharmaceutical composition for treating aberrant MASP-3 activity such as infections, cancer, MBL-deficiency, disorders of the immune system and reproductive system. The MASP-3 polypeptide is also used for treating diseases associated with human immunodeficiency virus, multiple sclerosis, myasthenia gravis, epilepsy, rheumatoid arthritis, vasculitis, autoimmune hemolytic anemia, Crohn's disease, asthma, diabetes, psoriasis, multiple myeloma, atherosclerosis etc. It is also
                                                      inflammatory condition related to complement activation through MBL/MASP complexes. MASP-3 is also useful for treating an inflammatory condition resulting from an autoimmune condition after acute myocardial infarction or brain ischemia. It is also useful for treating an individual suffering from a disorder resulting from an imbalanced cytokine network. The present sequence represents a DNA encoding a human MASP-3 polypeptide.
                                                                                                                                                                                                                                 diabetes, psoriasis, multiple myeloma, atherosclerosis etc. It is all useful for inhibiting activation of C4 complement by inhibiting the pathway, inhibiting MASP-2 activity, inhibiting or treating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides and polynucleotides encoding the protein, used for treating reoxygenated ischemic tissues, mannon-binding lectin deficiency, multiple sclerosis \,\cdot\,
   Sequence 3895 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a mannan-binding lectin (MBL) associated serine protease-3 (MASP-3) polypeptide. MASP-3 exerts an inhibitory effect on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 88-96; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the complement activation particularly when bound to MBL/MASP-2 complexes
952 A; 1068 C;
987 G; 888
   T; 0 other;
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RESULT 10
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                                                                                                                                             US-09-874-198-1 (1-41) x AAF83985
                                                                                                                                                                                 Query Match:
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                                                                                                                                                                                                         Percent Similarity:
AAF74442 standard;
                                                229 ACTTGGAATATCACTGTCCCAGATGGGTTTCGG
                                                                                             169 ATGTTTGGCCAGATCCAGTCGCCTGGTTATCCAGACTCCTATCCCAGTGATTCAGAGGTG
                                                                                                                   11 ValPheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArg
                                                                     31 ArgTrpThrLeuThrAlaProProGlyTyrArg
                                                                                                                                                                                              Similarity:
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 CDNA; 1988
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                                                                                                                                                                              Matches:
Conservative:
Mismatches:
Indels:
                                              261
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228 30

Human; PRO; PROX; cytostatic; immunomodulatory;
gene therapy; cell proliferation; differentiation

immune associated disorder; gestational disease; pre-clampsia;

proliferation; differentiation disorder;

reproduction;

Human PRO11 nucleotide sequence SEQ ID NO:21.

09-MAY-2001 AAF74442;

(first entry)

11-AUG-1999; 10-AUG-2000;

2000US-0148433

9908-0148433

(CURA-) CURAGEN CORP

11-AUG-2000; 2000WO-US21857

15-FEB-2001 WO200110902-A2 Homo sapiens.

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                     Human; PRO; PROX; cytostatic; immunomodulatory; reproduction;
gene therapy; cell proliferation; differentiation disorder; c
                                                                                                                                                                                                                                                                           09-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene
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11-AUG-1999;
                                 11-AUG-2000; 2000WO-US21857
                                                                                                                                                                                                                                           Human PRO9 nucleotide
                                                                                                                                                                                                                                                                                                            AAF74440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1384
                                                                 15-FEB-2001.
                                                                                                                                                                                                                                                                                                                                            AAF74440 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                504 TGTCACTGGCTGCTTGAGGCTCCTGAGGGCCAGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgArgTrpThrLeuThrAlaProProGlyTyrArg 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCACCACCGGCCGCATCGTCTCTCCAGGCTTCCCGGGCAACTACAGCAACAACCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGlu
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                                                                                                                                                                       associated disorder;
                                                                                                                                                                                                                                                                         (first entry)
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91.50
46.15%
40.38%
38.45%
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                                                                                                                                                                     gestational disease; pre-clampsia;
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Indels:
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21
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RESULT 12
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Best Local Similarity:
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder
                                                                                                    Human; PRO; PROX; cytostatic; immunomodulatory; reproduction; gene therapy; cell proliferation; differentiation disorder; carimmune associated disorder; gestational disease; pre-clampsia;
                                                                                                                                                                                                                                                                                                                            1504 TGTCACTGGCTGCTTGAGGCTCCTGAGGGCCCAGCGG 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 33-35; 166pp; English.
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                                             WO200110902-A2
                                                                                                                                                                    Human PRO10 nucleotide sequence SEQ ID NO:19.
                                                                                                                                                                                                                                                               AAF74441
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                                                                                                                                                                                                                                                                standard;
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38.45%
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Matches:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder
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                                                                                                                                                                                                                                                                                                                           1504 TGTCACTGGCTGCTTGAGGCTCCTGAGGGCCCAGCGG 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1384 CCCTTCTGGGATTCAAAGGAGCCCGTCTGCATCGCTGCTTGCGGCGGAGTGATCCGCAAT 1443
                                                                                     Human: PRO; PROX; cytostatic; immunomodulatory; reproduction;
gene therapy; cell proliferation; differentiation disorder; c
                                                                                                                                                                                 09-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                   1444
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10-AUG-2000; 2000US-0148433.
   WO200110902-A2
                                     Homo sapiens
                                                                                                                                           Human PRO12 nucleotide sequence SEQ
                                                                                                                                                                                                                                                      AAF74443 standard;
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                                                                                                                                                                                                                                                                                                                                                          ArgargTrpThrLeuThrAlaProProGlyTyrArg 41
                                                                                                                                                                                                                                                                                                                                                                                              GGCACCACCGGCCGCATCGTCTCCCAGGCTTCCCGGGCCAACTACAGCAACAACCTCACC 1503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Page 35-37; 166pp; English.
                                                                   associated disorder; gestational disease; pre-clampsia; ss.
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Conservative:
Mismatches:
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Best Local Similarity:
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          Human; PRO; PROX; cytostatic; immunomodulatory; reproduction; gene therapy; cell proliferation; differentiation disorder; cimmune associated disorder; gestational disease; pre-clampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17) properties have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a
                                                                                                                                                                                                                                                                                                                   medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder
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                                                                                                                 09-MAY-2001
                                                                                                                                                                                AAF74438 standard; cDNA; 3863
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PROX-associated disorder, e.g. cancer
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10-AUG-2000;
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DB; AAB70542.
                                                                                                                                                                                                                                                                        ArgArgTrpThrLeuThrAlaProProGlyTyrArg 41
                                                                                                                                                                                                                                                                                                                                                      -----PheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGlu
                                                                                 PRO7
                                                                               nucleotide sequence
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2000US-0148433
                                                                                                               (first entry)
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91.50
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Conservative:
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pre-clampsia;

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                         Human PRO8 nucleotide sequence SEQ ID NO:15
                                                   09-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 24-27; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding secreted polypeptides, designated PROX polypeptides, useful for treating a syndrome associated with a PROX-associated disorder, e.g. cancer -
                                                                           AAF74439;
                                                                                                   AAF74439 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention
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10-AUG-2000; 2000US-0148433
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3863 BP; 781 A; 1306 C; 1028 G; 747 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-AUG-2000; 2000WO-US21857
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                                                                                                                                                                                                                                                                                                                                       Match:
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                                                                                                                                                  TGTCACTGGCTGCTTGAGGCTCCTGAGGGCCAGCGG
                                                                                                                                                                                                                                                CCCATCTGGGATTCAAAGGAGCCCGTATGCATCGCTGCTTGCGGCGGAGTGATCCGCAAT 1443
                                                                                                                                                                                                 GCCACCACCGGCCGCATCGTCTCTCCAGGCTTCCCGGGCAACTACAGCAACAACCTCACC 1503
                                                                                                                                                                                                                         ----PheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGlu
                                                                                                                                                                       ArgArgTrpThrLeuThrAlaProProGlyTyrArg 41
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 PRO;
PROX; cytostatic; immunomodulatory; reproduction;
                                                  (first entry)
                                                                                                   cDNA; 3879
                                                                                                                                                                                                                                                                                                                          0.398
91.50
46.15%
40.38%
38.45%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  describes isolated nucleic acids encoding secreted ted PROX polypeptides (i.e. a PRO polypeptide where
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Indels:
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ABK28635
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            09-APR-2002
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                                     ABK28635;
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US-09-874-198-1 (1-41) x AAF74439 (1-3879)
                                                                                                                                                                                                                                      1504 TGTCACTGGCTGCTTGAGGCTCCTGAGGGCCAGCGG 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 28-31; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding secreted polypeptides, designated PRO polypeptides, useful for treating a syndrome associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-AUG-1999; 99US-0148433.
10-AUG-2000; 2000US-0148433.
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immune associated disorder; gestational disease; pre-clampsia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROX-associated disorder, e.g. cancer
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                                                                                                                                                                                                                                                                                           ArgArgTrpThrLeuThrAlaProProGlyTyrArg 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCATCTGGGATTCAAAGGAGCCCGTATGCATCGCTGCTTGCGGCGGAGTGATCCGCAAT 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProLysTrp-----ProGluProVal-----
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                                                                                                                                                                                                                                                                                                                                                         GCCACCACCGGCCGCATCGTCTCCCAGGCTTCCCGGGCCAACTACAGCAACAACCTCACC 1503
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                                                                                                                   standard;
(first entry)
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Indels:
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           designated PROX
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Human

cDNA encoding

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Query
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Best Local Similarity:
                                 US-09-874-198-1 (1-41)
                                                                                                                                                                   Alignment
                                                                                                                                                                                                                                          The invention relates to forty four human secreted proteins (referred to SECP-14) and the nucleic acids encoding them. Also included are a host cell transformed with the nucleic acid, a transgenic enimal comprising the nucleic acid, an anti-SECP antibody, use of the SECP proteins in isolating agonists and antagonists of SECP activity and a method of isolating compounds which alter the expression of the SECP nucleic acid. The SECP polynucleotides and CC polypeptides are useful in the diagnosis, treatment and prevention of CC cardiovascular (e.g. atherosclerosis, hypertension, myocardial CC infarction), autoimmune/inflammatory (e.g. acquired immunodeficiency syndrome (AIDS), allergies, rheumatoid arthritis), cell proliferative CC (e.g. cancer), developmental (e.g. Duchenne and Becker muscular CC disorders, Numerous other examples of each disorder are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2000; 2000US-212890P.
23-JUN-2000; 2000US-213466P.
27-JUN-2000; 2000US-214601P.
31-JUL-2000; 2000US-22372P.
08-SEP-2000; 2000US-231435P.
15-SEP-2000; 2000US-232889P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressive; antiviral; anti-HIV; antiarthritic; antirheumatic; muscular active general; anticonvulsant; nootropic; neuroprotective; antiallergic; hypotensive; cardiovascular disorder; atherosclerosis; hypertension; myocardial infarction; autoimmune disorder; hippertension; myocardial infarction; autoimmune disorder; inflammatory disorder; AIDS; acquired immunodeficiency syndrome; allergy; rheumatoid arthritis; cell proliferative disorder; cancer; developmental disorder; buchenne muscular dystrophy; neurological disorder; epilepsy; Alzheimer's disease.
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P-PSDB; AAU81976.
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                                                                                                                                                                                                                                     specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                   М
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                                                                                   Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rty four human secreted proteins (referred to as SECP-1 to SECP-44), eful in the diagnosis, treatment and prevention of cardiovascular eq. atherosclerosis), autoimmune/inflammatory (e.g. allergies) and
ProLysTrp----ProGluProVal---
                                                                                                                                                                     Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative disorders
                                                                                                                                                                                                    4034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Tang YT, Yue H, Ell
, Lal P, Xu Y, Warren
Batra S, Burford N, 
Gandhi AR, Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene;
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Warren BA, Hafali
Ford N, Yao MG, Ngu
Young J, Patterson
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                                                                                                                                                                                                    1062 G;
                                                                Gaps:
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Hafalia AJA,
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KW Huma

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                                                                                                                                                                                                                   Novel human SEZ6 polypeptide useful for inducing neural regeneration, inhibiting neural degeneration, preventing seizures, and for treating infertility, Alzheimer's disease, stroke, seizures, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; SEZ6; neural regeneration; seizure; infertility; gene therapy; stroke; Alzheimer's disease; Huntington's disease; myasthenia gravis; nootropic; neuroprotective; anticonvulsant; cerebroprotective; stroke; vasotropic; neuronal growth; growth factor-mediated chemotaxis; trauma; neurological disorder; muscular dystrophy; muscle injury; vulnerary; amyotropic lateral sclerosis; multiple sclerosis ischaemla; diabetes; epilepsy; Parkinson's disease; sexual development; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1337
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                                                                                                                                                                                                     infertility,
                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                                      Su EW;
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                                                                                                                                               Page 117-118; 127pp; English
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263..2749
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ID NO: 2 in (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human SEZ6 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mature hSEZ6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s region is specifically claimed claim 13 of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41
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growth, neurite outgrowth, neuronal regeneration, neuronal growth factor-mediated chemotaxis, altered behavioural patisleep or eating disorders and for treating neurological dis

The invention relates to an isolated human SEZ6 (hSEZ6) its corresponding DNA molecule. SEZ6 is useful for enhan

enhancing

neuronal

e.g.,

polypeptide survival,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-874-198-1 (1-41) x AAD25344 (1-4198)
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WPI; 2001-656860,
'P-PSDB; ABB66180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease. SEZ6 is useful for treating a patient suffering from a neurological disorder such as epilepsy, Alzhelmer's disease, Parkinson's disease, seizure related disorder or a disorder associated with stroke. SEZ6 DNA is useful as probes for gene mapping and for detecting transcription, translation and/or expression of hSEZ6 polypeptide in human tissue. A transgenic animal is useful as an animal model in research and drug development procedures, and for testing compounds or other treatment modalities which may prevent, suppress or cure a pathology or disease associated with hSEZ6 activities. SEZ6 is also useful for treating abnormal primary or secondary sexual development, e.g., impotence, infertility or reduced libido. The hSEZ6 polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL10283 standard; cDNA; 9455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as trigeminal neuralgia, Bell's palsy, myasthenia gravis, muscular dystrophy, muscle injury, invertebrate disk syndrome, thoracic outlet destruction syndrome, amyotropic lateral sclerosis, multiple sclerosis ischaemia associated with stroke, neuropathy associated with diabetes, spinal cord trauma, facial nerve crush and other trauma, Huntington's
                                                                                                                                                                              23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                     Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology;
                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster expressed polynucleotide SEQ ID NO 25331
                                                     Venter JC,
                                                                                                                         23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                   27-SEP-2001
                                                                                                                                                                                                                                                                                                                      pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL10283
                                                                                      (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4198 BP; 854 A; 1386 C; 1119 G; 839 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
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                  2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTCACTGGCTGCTTGAGGCTCCTGAGGGCCCAGCGG 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgArgTrpThrLeuThrAlaProProGlyTyrArg 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTTCTGGGATTCAAAGGAGCCCGTCTGCATCGCTGCTTGCGGCGGAGTGATCCGCAAT 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCACCACCGGCCGCATCGTCTCTCCAGGCTTCCCGGGCAACTACAGCAACAACCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProLysTrp-----ProGluProVal----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treating the above mentioned disorders by gene therapy s. The present sequence is human SEZ6 DNA.
                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.436
91.50
46.15%
40.38%
38.45%
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                                                     PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                     Myers
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Indels:
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                                                                                                                                                                                                                                                                                                                                       cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4198
21
3
13
15
                                                                                                                                                                                                                                                                                                                                          insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-874-198-1 (1-41) x ABL10283 (1-9455)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1738 GGCGTGCTGCGATCTCCGGGCTATCCTGGTCAGGCGCGGACCGGAACTCGACTGTCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid genes from Drosophila and interactions -
          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
                                                                                                                                                    23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                      P-PSDB; ABB66179
                                                                                                                         (PEKE
                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                           27-SEP-2001
                                                                                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                         pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster expressed polynucleotide SEQ ID NO 25328
                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL10282 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9455 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 25331; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrLeuThrAlaProProGlyTyrArg 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArgArgTrp
                                                                   2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAACTGACGGCGCCGTTTGGCTACCGG 1824
                                                                                                                         ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity:
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дс,
                                                                                                                         CORP
                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2333 A; 2397 C; 2484 G; 2241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA; 13036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.37
84.00
68.97%
55.17%
35.29%
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                                                                                             PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection reagent for detecting 1000 or more
                                                                                             Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
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interactions

Claim

1; SEQ ID NO 25328; 21pp + Sequence Listing; English

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGI76-ABL30511), expressed DNA sequences (ABLIGI76-ABL30511), expressed DNA sequences (ABLIGI76) and the encoded proteins

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The sequence data for this patent did not form specification, but was obtained in electronic i

but was obtained in electronic

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WIPO

(ABB57737-ABB72072)

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RESULT 20
ABK63805
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                                                                                                                             02-NOV-2000;
11-MAY-2001;
15-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                            3161
                                                                                                                                                                                                                                                                                  Rat sequence differentially expressed in response to a hepatotoxin #1712
                                                                                                                                                                                                 07-FEB-2002
                                                                                                                                                                                                                   WO200210453-A2
                                                                                                                                                                                                                                                        differential expression;
                                                                                                                                                                                                                                                                                                                                                                                    3221 CAACTGACGGCGCCGTTTGGCTACCGG 3247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ht Similarity:
Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13036
Predicting toxic effects of compounds or the progression of these toxic
                     WPI; 2002-241625/29
                                       Mendrick D,
                                                                                                  13-JUN-2001;
                                                                                                          06-JUN-2001;
                                                                                                                     22-MAY-2001;
                                                                                                                                                          31-JUL-2000;
                                                                                                                                                                             30-JUL-2001; 2001WO-US23872
                                                                                                                                                                                                                                      Rattus norvegicus
                                                                                                                                                                                                                                                                                                         18-JUN-2002
                                                                                                                                                                                                                                                                                                                             ABK63805
                                                                                                                                                                                                                                                                                                                                               ABK63805 standard; cDNA; 4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                             13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArgArgTrp
                                                                                                                                                                                                                                                                   ss; hepatotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                   ThrLeuThrAlaProProGlyTyrArg 41
                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGTGCTGCGATCTCCGGGCTATCCTGGTCAGGCGCGACCGGAACTCGACTGTCGCTGG 3220
                                                            GENE
                                                                                                        2000US-244880P.
2001US-290029P.
2001US-290645P.
2001US-292336P.
2001US-295798P.
                                                                                                                                                                                                                                                                                                        (first entry)
                                        Porter
                                                            LOGIC
                                                                               2001US-303459P
                                                                                       2001US-297457P
2001US-298884P
                                                                                                                                                          2000US-222040P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP;
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84.00
68.97%
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35.29%
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                                        WE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL10282 (1-13036)
                                                                                                                                                                                                                                                       expressed sequence tag; EST; drug screening;
on; centrilobular necrosis; steatosis.
                                       Johnson KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3058 C;
                                                                                                                                                                                                                                                                                                                                               ₿P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3137 G; 3352 T; 0 other;
                                       Castle
                                       ΑL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13036
                                       Elashoff MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                             32
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Sequence 4344 BP;

1035 A; 1099

C; 1103 G; 1107 T; 0 other;

changes in gene expression and for identifying toxicity markers in tissues or cell exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene The method can also be used to identify an agent which modulates the toxic response and predict cellular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, and a user interface to view the information used to present information identifying the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global expression in a tissue or cell sample exposed to the compound of two omore genes listed in the specification, where differential expression the genes is indicative of at least one toxic effect or progression. cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level of effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or sequence is an expressed sequence tag (EST) or cDNA derived from a gewhich is differentially expressed in response to a hepatotoxic agent. compounds or the progression of these The invention relates to methods for predicting toxic effects D No 1712; 239pp; English. toxic effects by determining of two or the

of

밁 δÃ 밁 δÃ Дb Percent Similarity: Best Local Similarity: US-09-874-198-1 (1-41) x ABK63805 (1-4344) Query Match: 2626 2566 GGTCCAGTTTGGACAAGTCCTCCTTTTGTAAACTATACTTGTGGAGGTTTCCTGACTGGA 2625 2686 TTGTGGAACATTGAAGTCCCAAACAACTACCGC 2718 NO . . 3 4 GlyProLysTrpProGluProValPhe-----CTCTCTGGGCAATTTTCTAGCCCATACTACCCTGGGAGCTATCCTAATAATGCCAGATGT ArgTrpThrLeuThrAlaProProGlyTyrArg 41 -----GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArg 4.02 83.50 41.18% 31.37% 35.08% Conservative: Mismatches: Indels: Matches: Length: 4344 16 5 17 13

12

Job time : 358 secs

Search completed: January 11,

2003, 11:16:24

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